

GenCore version 5.1.6
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leic search, using sw model

April 12, 2004, 16:22:07 ; Search time 916.308 Seconds

(without alignments)
912.511 Million cell updates/sec

US-10-090-326-23

1 agcatcatctctgcatggtcagggtcat 28

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

27513289 seqs, 14931090276 residues

hits satisfying chosen parameters: 203984

length: 0
length: 60

: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hco:*

9: gb_esti:*

10: gb_est2:*

11: gb_hco:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

is the number of results predicted by chance to have a
ater than or equal to the score of the result being printed,
rived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
60.7	46	9	AV948819	AV948819	AV948819 AV948819
57.1	49	9	AI762609	AI762609	AI762609 w156d08.x
56.4	57	14	D71055	D71055	D71055 CELK061E3R
54.3	59	14	CB058981	CB058981	CB058981 NISC_jx10

60	10	AM458816	AM458816	AM458816
27	12	BM396377	BM396377	BM396377
49	9	AA515410	AA515410	AA515410
51	29	CC515838	CC515838	CC515838
55	28	BZ763116	BZ763116	BZ763116
36	28	AZ591147	AZ591147	AZ591147
39	28	AZ635338	AZ635338	AZ635338
50	28	AZ330881	AZ330881	AZ330881
58	9	AL651765	AL651765	AL651765
58	29	GGA320139	GGA320139	GGA320139
52	9	AA489521	AA489521	AA489521
52	9	AA492773	AA492773	AA492773
53	28	AZ922240	AZ922240	AZ922240
56	29	LBFA030DI2	LBFA030DI2	LBFA030DI2
50	9	AU106538	AU106538	AU106538
51	14	CB260365	CB260365	CB260365
55	28	AZ789849	AZ789849	AZ789849
57	28	BH911716	BH911716	BH911716
59	29	CG869799	CG869799	CG869799
37	28	AZ824496	AZ824496	AZ824496
46	29	CG426656	CG426656	CG426656
49	9	AI670113	AI670113	AI670113
52	13	BQ086305	BQ086305	BQ086305
53	28	BZ661820	BZ661820	BZ661820
53	28	BZ661823	BZ661823	BZ661823
57	14	CB217728	CB217728	CB217728
58	9	AI952050	AI952050	AI952050
58	14	CA337713	CA337713	CA337713
59	14	CF842268	CF842268	CF842268
60	14	CD956570	CD956570	CD956570
30	28	AZ456409	AZ456409	AZ456409
31	28	BH906192	BH906192	BH906192
31	28	BH906199	BH906199	BH906199
42	29	AL765117	AL765117	AL765117
46	14	H92446	H92446	H92446
55	29	CC513990	CC513990	CC513990
55	9	AU014183	AU014183	AU014183
55	29	CG782946	CG782946	CG782946
29	14	CA797153	CA797153	CA797153
37	9	AI442882	AI442882	AI442882
39	28	AZ419652	AZ419652	AZ419652
41	13	C52224	C52224	C52224
51	29	AL754099	AL754099	AL754099
52	29	AL943090	AL943090	AL943090
57	9	AL797516	AL797516	AL797516
57	28	CC056995	CC056995	CC056995
58	9	AA931854	AA931854	AA931854
32	14	RI5883	RI5883	RI5883
33	9	AU243251	AU243251	AU243251
40	9	AI377260	AI377260	AI377260
40	9	AV834452	AV834452	AV834452
41	28	BH848702	BH848702	BH848702
44	28	AZ430558	AZ430558	AZ430558
46	9	AI250491	AI250491	AI250491
50	9	AU104937	AU104937	AU104937
50	9	AU104938	AU104938	AU104938
50	9	AU104939	AU104939	AU104939
50	9	AU104940	AU104940	AU104940
50	9	AU104941	AU104941	AU104941
50	9	AU104943	AU104943	AU104943
50	29	BX892187	BX892187	BX892187
52	29	CG720139	CG720139	CG720139
53	9	AL958295	AL958295	AL958295
54	10	AW781356	AW781356	AW781356
55	9	AA917476	AA917476	AA917476
55	14	H44869	H44869	H44869
57	12	BM433543	BM433543	BM433543
58	29	CG714576	CG714576	CG714576
60	14	CF845319	CF845319	CF845319
37	9	AA647854	AA647854	AA647854
42	29	BX894509	BX894509	BX894509
46	9	AA932378	AA932378	AA932378
46	9	AA561123	AA561123	AA561123

45.7	46	29	BX649708	BX649708 Arabidops	c 151	12.2	43.6	49	9	AA387830	AA387830
45.7	51	14	CA335447	CA335447 NISC lt11	c 152	12.2	43.6	49	29	CNS07F1F	AL60789
45.7	53	9	AL870437	AL870437 Arabidops	c 153	12.2	43.6	50	9	AUI02476	AUI02476
45.7	53	14	CB409427	CB409427 NISC nc05	c 154	12.2	43.6	50	9	AUI02687	AUI02687
45.7	53	14	CB410615	CB410615 NISC nc12	c 155	12.2	43.6	50	9	AUI02688	AUI02688
45.7	54	14	CD029902	CD029902 NISC nc12	c 156	12.2	43.6	50	9	AUI02689	AUI02689
45.7	56	9	AV674710	AV674710 Arabidops	c 157	12.2	43.6	50	9	AUI02690	AUI02690
45.7	56	28	BH221475	BH221475 Arabidops	c 158	12.2	43.6	50	9	AUI02695	AUI02695
45.7	56	28	BH638481	BH638481 Arabidops	c 159	12.2	43.6	50	9	AUI02697	AUI02697
45.7	56	28	BH651948	BH651948 Arabidops	c 160	12.2	43.6	50	9	AUI02698	AUI02698
45.7	57	28	AZ915988	AZ915988 Arabidops	c 161	12.2	43.6	50	9	AUI02700	AUI02700
45.7	58	14	CA336852	CA336852 NISC lv06	c 162	12.2	43.6	50	9	AUI03187	AUI03187
45.7	60	14	CD948943	CD948943 Arabidops	c 163	12.2	43.6	50	9	AUI04155	AUI04155
45.7	60	14	CD948943	CD948943 Arabidops	c 164	12.2	43.6	50	9	AUI06406	AUI06406
45.0	30	28	AZ800842	AZ800842 Arabidops	c 165	12.2	43.6	50	9	AUI06468	AUI06468
45.0	37	9	AI544907	AI544907 Arabidops	c 166	12.2	43.6	50	9	AUI06529	AUI06529
45.0	41	14	T54451	T54451 Arabidops	c 167	12.2	43.6	50	9	AUI06541	AUI06541
45.0	47	14	H55642	H55642 Arabidops	c 168	12.2	43.6	50	9	AUI06866	AUI06866
45.0	47	28	AZ797405	AZ797405 Arabidops	c 169	12.2	43.6	51	12	BG677901	BG677901
45.0	49	9	AI120408	AI120408 Arabidops	c 170	12.2	43.6	51	28	AZ309542	AZ309542
45.0	49	9	AI931127	AI931127 Arabidops	c 171	12.2	43.6	52	9	AI925247	AI925247
45.0	49	29	CG869123	CG869123 Arabidops	c 172	12.2	43.6	52	14	CB377176	CB377176
45.0	50	12	BM532066	BM532066 Arabidops	c 173	12.2	43.6	52	14	T74264	T74264
45.0	54	13	BU765480	BU765480 Arabidops	c 174	12.2	43.6	53	10	BF507141	BF507141
45.0	57	12	CA850749	CA850749 Arabidops	c 175	12.2	43.6	54	29	LBAP042D08	LBAP042D08
45.0	57	12	BU036242	BU036242 Arabidops	c 176	12.2	43.6	55	13	BQ254913	BQ254913
45.0	60	14	CF116097	CF116097 Arabidops	c 177	12.2	43.6	56	9	AA795227	AA795227
44.3	29	28	AZ847949	AZ847949 Arabidops	c 178	12.2	43.6	56	29	BX199129	BX199129
44.3	33	29	TA122E04P	TA122E04P Arabidops	c 179	12.2	43.6	57	28	BH905200	BH905200
44.3	35	14	N73542	N73542 Arabidops	c 180	12.2	43.6	58	9	AI657773	AI657773
44.3	36	28	AZ769773	AZ769773 Arabidops	c 181	12.2	43.6	58	9	AA542007	AA542007
44.3	36	28	CC057367	CC057367 Arabidops	c 182	12.2	43.6	58	13	BQ264668	BQ264668
44.3	38	28	AZ501000	AZ501000 Arabidops	c 183	12.2	43.6	58	14	H55568	H55568
44.3	38	29	BX534430	BX534430 Arabidops	c 184	12.2	43.6	59	29	TA31G03P	TA31G03P
44.3	39	29	BX893335	BX893335 Arabidops	c 185	12.2	43.6	60	12	BM023389	BM023389
44.3	44	9	AW063999	AW063999 Arabidops	c 186	12.2	43.6	60	13	BQ264424	BQ264424
44.3	46	28	AZ429958	AZ429958 Arabidops	c 187	12.2	43.6	60	13	BQ264650	BQ264650
44.3	46	28	AZ840663	AZ840663 Arabidops	c 188	12.2	43.6	60	13	BQ264651	BQ264651
44.3	47	14	T98319	T98319 Arabidops	c 189	12.2	43.6	60	13	BQ264651	BQ264651
44.3	48	12	BG684299	BG684299 Arabidops	c 190	12.2	43.6	60	13	BQ264651	BQ264651
44.3	48	29	AL944927	AL944927 Arabidops	c 191	12.2	43.6	60	13	BQ264651	BQ264651
44.3	50	9	AUI02400	AUI02400 Arabidops	c 192	12.2	43.6	60	13	BQ264651	BQ264651
44.3	50	12	BG405996	BG405996 Arabidops	c 193	12.2	43.6	60	13	BQ264651	BQ264651
44.3	52	9	CB219037	CB219037 Arabidops	c 194	12.2	43.6	60	13	BQ264651	BQ264651
44.3	52	9	A1942762	A1942762 Arabidops	c 195	12.2	43.6	60	13	BQ264651	BQ264651
44.3	52	10	BF643549	BF643549 Arabidops	c 196	12.2	43.6	60	13	BQ264651	BQ264651
44.3	52	28	BH621150	BH621150 Arabidops	c 197	12.2	43.6	60	13	BQ264651	BQ264651
44.3	53	9	AV833296	AV833296 Arabidops	c 198	12.2	43.6	60	13	BQ264651	BQ264651
44.3	53	28	BH621149	BH621149 Arabidops	c 199	12.2	43.6	60	13	BQ264651	BQ264651
44.3	55	14	CB217964	CB217964 Arabidops	c 200	12.2	43.6	60	13	BQ264651	BQ264651
44.3	56	28	AZ785606	AZ785606 Arabidops	c 201	12.2	43.6	60	13	BQ264651	BQ264651
44.3	57	14	CA335631	CA335631 Arabidops	c 202	12.2	43.6	60	13	BQ264651	BQ264651
44.3	57	28	CC456224	CC456224 Arabidops	c 203	12.2	43.6	60	13	BQ264651	BQ264651
44.3	58	9	AA288434	AA288434 Arabidops	c 204	12.2	43.6	60	13	BQ264651	BQ264651
44.3	58	9	AA541299	AA541299 Arabidops	c 205	12.2	43.6	60	13	BQ264651	BQ264651
44.3	59	14	CA337764	CA337764 Arabidops	c 206	12.2	43.6	60	13	BQ264651	BQ264651
44.3	59	28	AZ642800	AZ642800 Arabidops	c 207	12.2	43.6	60	13	BQ264651	BQ264651
44.3	60	12	BG272272	BG272272 Arabidops	c 208	12.2	43.6	60	13	BQ264651	BQ264651
44.3	60	29	BX534432	BX534432 Arabidops	c 209	12.2	43.6	60	13	BQ264651	BQ264651
44.3	62	29	CC887559	CC887559 Arabidops	c 210	12.2	43.6	60	13	BQ264651	BQ264651
43.6	37	9	AA913126	AA913126 Arabidops	c 211	12.2	43.6	60	13	BQ264651	BQ264651
43.6	37	9	AA958086	AA958086 Arabidops	c 212	12.2	43.6	60	13	BQ264651	BQ264651
43.6	37	28	BH790463	BH790463 Arabidops	c 213	12.2	43.6	60	13	BQ264651	BQ264651
43.6	39	9	AV834166	AV834166 Arabidops	c 214	12.2	43.6	60	13	BQ264651	BQ264651
43.6	40	9	AA958439	AA958439 Arabidops	c 215	12.2	43.6	60	13	BQ264651	BQ264651
43.6	40	9	AI796152	AI796152 Arabidops	c 216	12.2	43.6	60	13	BQ264651	BQ264651
43.6	40	9	AA575251	AA575251 Arabidops	c 217	12.2	43.6	60	13	BQ264651	BQ264651
43.6	40	12	BH821604	BH821604 Arabidops	c 218	12.2	43.6	60	13	BQ264651	BQ264651
43.6	43	9	AA328331	AA328331 Arabidops	c 219	12.2	43.6	60	13	BQ264651	BQ264651
43.6	45	28	CC049880	CC049880 Arabidops	c 220	12.2	43.6	60	13	BQ264651	BQ264651
43.6	45	28	CC860807	CC860807 Arabidops	c 221	12.2	43.6	60	13	BQ264651	BQ264651
43.6	46	9	AA902889	AA902889 Arabidops	c 222	12.2	43.6	60	13	BQ264651	BQ264651
43.6	47	29	TA77F02P	TA77F02P Arabidops	c 223	12.2	43.6	60	13	BQ264651	BQ264651

42.9	50	9	AU102483	AU102483	AU102483	297	11.8	42.1	53	28	BH892483	BH892483
42.9	50	9	AU104870	AU104870	AU104870	298	11.8	42.1	54	28	B34737	B34737
42.9	50	9	AU105585	AU105585	AU105585	299	11.8	42.1	55	9	AI091130	AI091130
42.9	50	9	AU105586	AU105586	AU105586	300	11.8	42.1	56	14	CB256599	CB256599
42.9	50	9	AU106344	AU106344	AU106344	301	11.8	42.1	57	14	CA795292	CA795292
42.9	50	9	AU106794	AU106794	AU106794	302	11.8	42.1	57	28	BH758271	BH758271
42.9	50	9	AU106795	AU106795	AU106795	303	11.8	42.1	58	9	AA643598	AA643598
42.9	50	14	CA338100	CA338100	NISC_lw10	304	11.8	42.1	58	29	CG987730	CG987730
42.9	50	28	AZ332306	AZ332306	IM0060B18	305	11.8	42.1	60	9	AI047804	AI047804
42.9	51	13	BQ239145	BQ239145	TA05036F	306	11.8	42.1	60	28	AI906209	AI906209
42.9	51	29	CG718276	CG718276	1119052C1	307	11.8	42.1	60	28	CC200308	CC200308
42.9	52	9	AA208481	AA208481	mv85a07.r	308	11.6	41.4	23	28	AZ354268	AZ354268
42.9	52	9	AA274507	AA274507	v802402.r	309	11.6	41.4	25	28	AZ417175	AZ417175
42.9	52	10	BF643664	BF643664	NP007G12E	310	11.6	41.4	26	29	TA24G03P	TA24G03P
42.9	52	14	CB410529	CB410529	NISC_nc12	311	11.6	41.4	28	9	AA337024	AA337024
42.9	52	28	BZ662155	BZ662155	SALK_0256	312	11.6	41.4	32	14	T77145	T77145
42.9	53	28	AZ775134	AZ775134	2M0007L11	313	11.6	41.4	34	9	AA984692	AA984692
42.9	53	28	BZ662624	BZ662624	SALK_0261	314	11.6	41.4	34	9	AU268597	AU268597
42.9	54	14	CA337584	CA337584	NISC_lw03	315	11.6	41.4	36	28	AZ609522	AZ609522
42.9	54	28	AQ026226	AQ026226	1(3)07615	316	11.6	41.4	36	29	BX534333	BX534333
42.9	54	28	BH414183	BH414183	1007036G0	317	11.6	41.4	37	9	AA322819	AA322819
42.9	55	12	BG811905	BG811905	doc02a06	318	11.6	41.4	38	28	AZ758198	AZ758198
42.9	55	14	CD029926	CD029926	mgmk004XM	319	11.6	41.4	38	28	BH755669	BH755669
42.9	56	9	AL800323	AL800323	AL800323	320	11.6	41.4	40	9	AA642607	AA642607
42.9	56	14	CA337917	CA337917	NISC_lw08	321	11.6	41.4	40	9	AI041512	AI041512
42.9	56	14	CB297028	CB297028	12B22056	322	11.6	41.4	40	9	AA579743	AA579743
42.9	57	10	AW641265	AW641265	cm05c05.w	323	11.6	41.4	40	28	AZ604737	AZ604737
42.9	57	28	BH805522	BH805522	1008061A0	324	11.6	41.4	40	28	BH902530	BH902530
42.9	57	28	BH906438	BH906438	SALK_0333	325	11.6	41.4	42	29	BX651245	BX651245
42.9	58	9	AA937412	AA937412	0103f05.s	326	11.6	41.4	43	9	AA862169	AA862169
42.9	58	9	AI147450	AI147450	Q961dl1.r	327	11.6	41.4	43	28	AZ588360	AZ588360
42.9	58	28	AZ922051	AZ922051	HRC02D10	328	11.6	41.4	43	28	AZ875350	AZ875350
42.9	59	9	AA071902	AA071902	mm71604.r	329	11.6	41.4	44	14	CA796716	CA796716
42.9	60	10	BF506850	BF506850	10J22P67	330	11.6	41.4	45	28	BH854731	BH854731
42.1	27	28	AZ626851	AZ626851	1M04670J3	331	11.6	41.4	47	12	BQ064943	BQ064943
42.1	28	28	AZ632301	AZ632301	1M0486C23	332	11.6	41.4	47	14	CF337893	CF337893
42.1	29	28	AZ623371	AZ623371	1M0460003	333	11.6	41.4	47	28	AZ581261	AZ581261
42.1	31	28	BF685654	BF685654	602140521	334	11.6	41.4	47	28	AZ804115	AZ804115
42.1	31	28	AZ945327	AZ945327	2M0206J09	335	11.6	41.4	50	9	AI040411	AI040411
42.1	32	28	AZ859128	AZ859128	2M0164B12	336	11.6	41.4	50	9	AI040461	AI040461
42.1	32	28	AZ899961	AZ899961	2M0273D03	337	11.6	41.4	50	28	AI08031	AI08031
42.1	34	28	AZ309524	AZ309524	1M0013104	338	11.6	41.4	50	28	BH227672	BH227672
42.1	36	10	AW245681	AW245681	2822809.5	339	11.6	41.4	50	28	BH789906	BH789906
42.1	36	28	AZ627044	AZ627044	2M0103A13	340	11.6	41.4	50	28	CC024195	CC024195
42.1	40	9	AJ239824	AJ239824	AJ239824	341	11.6	41.4	51	29	AL944876	AL944876
42.1	44	9	AU264623	AU264623	AU264623	342	11.6	41.4	52	9	AI2040424	AI2040424
42.1	45	14	T69111	T69111	yc31h09.r1	343	11.6	41.4	52	9	AI332999	AI332999
42.1	46	14	CF291149	CF291149	14ROOT--0	344	11.6	41.4	52	10	BF633916	BF633916
42.1	46	28	AZ459047	AZ459047	IM0263F07	345	11.6	41.4	52	14	CB217552	CB217552
42.1	47	9	AV833049	AV833049	AV833049	346	11.6	41.4	52	14	R05651	R05651
42.1	47	29	BX659718	BX659718	Arabidops	347	11.6	41.4	52	14	T93299	T93299
42.1	48	28	BH847205	BH847205	SALK_0445	348	11.6	41.4	52	28	B36269	B36269
42.1	48	28	CC024575	CC024575	3591_l_3	349	11.6	41.4	52	28	BH814586	BH814586
42.1	48	29	TA254C04P	TA254C04P	bruce1	350	11.6	41.4	52	29	CG893337	CG893337
42.1	49	9	AA19129	AA19129	z34a10.r	351	11.6	41.4	53	10	BF507246	BF507246
42.1	49	28	AZ373724	AZ373724	1M0126C05	352	11.6	41.4	53	29	AL944410	AL944410
42.1	50	9	AU104274	AU104274	AU104274	353	11.6	41.4	54	9	AI159446	AI159446
42.1	50	9	AU106540	AU106540	AU106540	354	11.6	41.4	54	14	CA797539	CA797539
42.1	50	9	AU107152	AU107152	AU107152	355	11.6	41.4	54	14	CF297053	CF297053
42.1	50	9	AU107153	AU107153	AU107153	356	11.6	41.4	54	14	CF859400	CF859400
42.1	50	9	AU107271	AU107271	AU107271	357	11.6	41.4	54	28	AZ416838	AZ416838
42.1	50	12	BG217170	BG217170	na52e08.	358	11.6	41.4	54	29	CG869495	CG869495
42.1	50	29	CA93346	CA93346	CH240_327	359	11.6	41.4	55	9	AA915742	AA915742
42.1	51	12	B1526968	B1526968	602927158	360	11.6	41.4	55	9	AI808781	AI808781
42.1	51	29	CNS07FF3	CNS07FF3	ANopheles	361	11.6	41.4	55	9	AI04102	AI04102
42.1	52	9	AI973612	AI973612	sd07c05.y	362	11.6	41.4	55	12	BG607617	BG607617
42.1	52	10	BE316749	BE316749	NF066E04L	363	11.6	41.4	55	28	BH910678	BH910678
42.1	52	13	BQ570298	BQ570298	g1147f10.	364	11.6	41.4	56	12	BG160532	BG160532
42.1	52	14	CB056129	CB056129	NISC_jj13	365	11.6	41.4	56	13	BX732612	BX732612
42.1	52	28	AZ658081	AZ658081	1M0534I08	366	11.6	41.4	56	28	AZ633063	AZ633063
42.1	53	14	CF291128	CF291128	14ROOT--0	367	11.6	41.4	57	28	AZ434302	AZ434302
42.1	53	28	B06520	B06520	CSRL-81f2-u	368	11.6	41.4	57	28	BH640783	BH640783
42.1	53	28				369	11.6	41.4	58	9	AA056749	AA056749

41.4	58	9	AI093609	ou82d05.s	C 443	11.4	40.7	58	14	CF844186	CP84418
41.4	58	10	BE213008	IPBrn0135	C 444	11.4	40.7	58	28	AZ592089	AZ59208
41.4	58	14	CB274168	mai89f05.	C 445	11.4	40.7	58	29	CG869466	CG86946
41.4	58	28	BZ590895	3590.1.80	C 446	11.4	40.7	59	9	AL872973	AL87297
41.4	58	29	CC494133	CH240.329	C 447	11.4	40.7	59	12	BI522115	BI52211
41.4	58	29	CG247451	1119082E0	C 448	11.4	40.7	59	12	BM863229	BM86322
41.4	58	29	CG247451	1119082E0	C 449	11.4	40.7	59	28	CC455113	CC45511
41.4	59	12	BG162461	dfl15a08.y	C 450	11.4	40.7	59	29	AL938470	AL93847
41.4	59	14	CB218879	NISC nb11	C 451	11.4	40.7	60	9	AI308953	AI30895
41.4	59	28	AZ341873	1M0074M06	C 452	11.4	40.7	60	14	T24473	T24473
41.4	59	29	BX656294	ArabiDops	C 453	11.2	40.0	23	12	BM397206	BM39720
41.4	59	29	CNS04589	TetraDops	C 454	11.2	40.0	24	28	AZ825913	AZ82591
41.4	60	10	BF611841	dfl15g07.y	C 455	11.2	40.0	26	28	AZ441490	AZ44149
41.4	60	12	BI941096	dfl14c06.y	C 456	11.2	40.0	26	28	BZ358973	BZ35897
41.4	60	28	AZ507903	1M0349G13	C 457	11.2	40.0	30	28	AZ309878	AZ30987
41.4	60	28	BH770466	LIMgtag23	C 458	11.2	40.0	30	28	AZ791321	AZ79132
41.4	60	29	CG986097	CH240.156	C 459	11.2	40.0	33	29	AL945047	AL94504
41.4	60	29	BX003621	ArabiDops	C 460	11.2	40.0	34	12	BM399526	BM39952
41.4	60	28	AZ490638	1M0323B13	C 461	11.2	40.0	34	28	AZ623317	AZ62331
41.4	60	28	AZ490638	1M0323B13	C 462	11.2	40.0	34	28	BH865029	BH86502
41.4	60	28	AZ471002	1M0285E03	C 463	11.2	40.0	34	28	CC179479	CC17947
41.4	60	28	AZ840905	2M0138H09	C 464	11.2	40.0	37	28	BZ379866	BZ37986
41.4	60	29	AA641517	nt62e09.s	C 465	11.2	40.0	37	28	DME547235	DME5472
41.4	60	29	CF298165	7LEAF--01	C 466	11.2	40.0	39	12	BI223730	BI22373
41.4	60	29	AI188860	q227a10.x	C 467	11.2	40.0	39	14	U44319	U44319
41.4	60	29	BX082844	BU082844	C 468	11.2	40.0	39	28	BH907039	BH90703
41.4	60	29	U19678	DRU19678.2e	C 469	11.2	40.0	40	9	AA683599	AA68359
41.4	60	29	AZ592386	1M0403H15	C 470	11.2	40.0	40	9	AI020727	AI02072
41.4	60	29	BH862997	SALK.0929	C 471	11.2	40.0	40	9	AI459438	AI45943
41.4	60	29	AZ511031	1M0355F20	C 472	11.2	40.0	40	9	AJ237265	AJ23726
41.4	60	29	AU052705	AU052705	C 473	11.2	40.0	40	12	BQ066312	BQ06631
41.4	60	29	AZ799531	2M0057M04	C 474	11.2	40.0	40	28	AZ335587	AZ33558
41.4	60	29	AZ593297	1M0404D16	C 475	11.2	40.0	40	28	CC025427	CC02542
41.4	60	29	BZ352916	SALK.1194	C 476	11.2	40.0	41	28	AL766232	AL76623
41.4	60	29	AA912398	q199c11.s	C 477	11.2	40.0	42	28	AZ592676	AZ59267
41.4	60	29	AI356141	qV52h04.x	C 478	11.2	40.0	43	9	AA663711	AA66371
41.4	60	29	R85401	VQ22a03.sl	C 479	11.2	40.0	43	14	W62611	W62611
41.4	60	29	AZ762556	1M0537M01	C 480	11.2	40.0	43	29	AG206053	AG20605
41.4	60	29	CC178649	RST188.Ba	C 481	11.2	40.0	43	29	BX891475	BX89147
41.4	60	29	CC455620	SALK.0850	C 482	11.2	40.0	44	14	D67718	D67718
41.4	60	29	W25663	zc64e08.r1	C 483	11.2	40.0	44	14	H54222	H54222
41.4	60	29	AZ949937	2M0213F18	C 484	11.2	40.0	44	28	BH862713	BH86271
41.4	60	29	AZ307696	1M0009G04	C 485	11.2	40.0	45	10	BE382645	BE38264
41.4	60	29	AI580559	tb70d01.x	C 486	11.2	40.0	45	29	BX002065	BX00206
41.4	60	29	AA531890	TG8STzz32	C 487	11.2	40.0	46	9	AI006918	AI00691
41.4	60	29	R78378	yi78d11.sl	C 488	11.2	40.0	46	9	AL585781	AL58578
41.4	60	29	T11101	hbc668.Huma	C 489	11.2	40.0	46	14	H72220	H72220
41.4	60	29	AU102283	AU102283	C 490	11.2	40.0	46	14	R39433	R39433
41.4	60	29	AU103943	AU103943	C 491	11.2	40.0	46	28	BH910965	BH91096
41.4	60	29	AU107115	AU107115	C 492	11.2	40.0	47	14	CF330472	CF33047
41.4	60	29	BX660472	ArabiDops	C 493	11.2	40.0	47	29	CG780418	CG78041
41.4	60	29	CB212627	OML02907	C 494	11.2	40.0	48	9	AA930873	AA93087
41.4	60	29	AZ812952	2M0080E01	C 495	11.2	40.0	48	9	AI172854	AI17285
41.4	60	29	BE321037	NF033H04R	C 496	11.2	40.0	48	9	AA386692	AA38669
41.4	60	29	BM023092	ie79c01.x	C 497	11.2	40.0	48	28	AZ442808	AZ44280
41.4	60	29	BQ400170	NTSC.m07	C 498	11.2	40.0	48	28	CC249527	CC24952
41.4	60	29	CA334971	NISC.lt04	C 499	11.2	40.0	49	14	CB277333	CB27733
41.4	60	29	H37883	yp57g06.r1	C 500	11.2	40.0	49	28	AZ601892	AZ60189
41.4	60	29	U38140	OSU38140.FD	C 501	11.2	40.0	49	29	BX546641	BX54664
41.4	60	29	AZ776478	2M0010E07	C 502	11.2	40.0	49	29	AI102696	AI10269
41.4	60	29	AZ802331	2M0061M08	C 503	11.2	40.0	50	9	AI103188	AI10318
41.4	60	29	CA839023	MCT022H11	C 504	11.2	40.0	50	9	AU104211	AU10421
41.4	60	29	AG233518	Locus.cor	C 505	11.2	40.0	50	9	AU105637	AU10563
41.4	60	29	AL938469	ArabiDops	C 506	11.2	40.0	50	9	AI106544	AI10654
41.4	60	29	AZ306177	1M0007G11	C 507	11.2	40.0	50	9	AI106786	AI10678
41.4	60	29	AA995974	osl3e08.s	C 508	11.2	40.0	50	9	AI106790	AI10679
41.4	60	29	AA393943	zt78a02.r	C 509	11.2	40.0	50	9	AU106791	AU10679
41.4	60	29	AA618428	ng03f10.s	C 510	11.2	40.0	50	9	AU107924	AU10792
41.4	60	29	CB910375	VVD177E01	C 511	11.2	40.0	50	9	AU107925	AU10792
41.4	60	29	H55330	CHR220269.C	C 512	11.2	40.0	50	9	AU107928	AU10792
41.4	60	29	AZ792680	2M0045118	C 513	11.2	40.0	50	14	CA301862	CA30186
41.4	60	29	BH856937	SALK.0775	C 514	11.2	40.0	50	14	CF063684	CF06368
41.4	60	29	BZ762334	SALK_0994	C 515	11.2	40.0	50	14	CF063684	CF06368
41.4	60	29	AI331551	fa94b12.y	C 515	11.2	40.0	50	14	CF063684	CF06368

[illegible]

[illegible]

38.6	56	28	BH791923	BH791923 SALK_0620	C 881	10.6	37.9	25	29	CC885336	CC885336
38.6	56	28	BZ761774	BZ761774 SALK_0812	882	10.6	37.9	26	28	AZ313876	AZ313876
38.6	56	28	BZ764389	BZ764389 SALK_1245	C 883	10.6	37.9	26	28	BH810744	BH810744
38.6	56	28	CC605056	CC605056 EY0325-3	884	10.6	37.9	26	29	TA129A07P	TA129A07P
38.6	56	29	BX655720	BX655720 Arabidops	C 885	10.6	37.9	28	9	AT471841	AT471841
38.6	56	29	BAF031H02	BX544154 Leishman	886	10.6	37.9	29	9	AU256137	AU256137
38.6	57	9	AA889441	AA889441 aj1h04.s	887	10.6	37.9	29	28	AZ309154	AZ309154
38.6	57	9	AL595919	AL595919 AL595919	888	10.6	37.9	30	12	BM395434	BM395434
38.6	57	12	BG173482	BG173482 602335795	889	10.6	37.9	31	9	AA581300	AA581300
38.6	57	14	D45775	D45775 HUMS02987	C 890	10.6	37.9	31	28	AZ605943	AZ605943
38.6	57	28	AZ333311	AZ333311 IM0062P15	C 891	10.6	37.9	31	28	BZ381841	BZ381841
38.6	57	28	AZ640607	AZ640607 IM0502011	C 892	10.6	37.9	31	29	AL984837	AL984837
38.6	57	28	BZ761724	BZ761724 SALK_0751	893	10.6	37.9	32	28	AZ662474	AZ662474
38.6	57	29	CG733686	CG733686 1119158E0	C 894	10.6	37.9	32	28	BH854494	BH854494
38.6	57	29	BX289656	BX289656 Arabidops	C 895	10.6	37.9	33	12	BM398846	BM398846
38.6	57	29	BX894722	BX894722 Arabidops	896	10.6	37.9	33	14	H23694	H23694
38.6	57	29	TA184E08P	AL474749 T. brucei	897	10.6	37.9	33	28	AZ363372	AZ363372
38.6	57	29	TA265D09P	AL484847 T. brucei	898	10.6	37.9	34	9	AA707825	AA707825
38.6	58	9	AA706604	AA706604 ah26b04.s	899	10.6	37.9	34	9	AA436781	AA436781
38.6	58	9	A1942620	A1942620 fc73f12.y	900	10.6	37.9	34	28	AZ592538	AZ592538
38.6	58	9	AA253796	AA253796 mw05b01.r	901	10.6	37.9	35	28	AZ821491	AZ821491
38.6	58	9	AA620451	AA620451 ae58d02.s	C 902	10.6	37.9	35	28	AZ838284	AZ838284
38.6	58	10	BH122763	BH122763 23_07rev	C 903	10.6	37.9	35	28	AZ938626	AZ938626
38.6	58	13	BQ590752	BQ590752 E012599-0	904	10.6	37.9	35	28	CC053541	CC053541
38.6	58	13	BQ784137	BQ784137 in10904.y	C 905	10.6	37.9	36	10	AW247788	AW247788
38.6	58	14	R68613	R68613 y106b11.s1	906	10.6	37.9	36	28	AZ338246	AZ338246
38.6	59	9	AA666844	AA666844 vm65g11.s	907	10.6	37.9	36	28	AZ345461	AZ345461
38.6	59	12	BG315025	BG315025 OP3_0.127	908	10.6	37.9	36	28	AZ486331	AZ486331
38.6	59	12	BQ551355	BQ551355 sad37a01.	C 909	10.6	37.9	36	28	AZ491747	AZ491747
38.6	59	13	BQ270424	BQ270424 ik10h06.y	C 910	10.6	37.9	36	28	BH906165	BH906165
38.6	59	14	CD007347	CD007347 VVB076E08	C 911	10.6	37.9	36	29	TA61A06Q	TA61A06Q
38.6	59	14	CD714565	CD714565 VVB202D09	C 912	10.6	37.9	37	12	B1695409	B1695409
38.6	59	14	CD716430	CD716430 VVB128E06	C 913	10.6	37.9	37	28	AZ838465	AZ838465
38.6	59	28	BH631194	BH631194 1007074G0	C 914	10.6	37.9	37	28	BZ592623	BZ592623
38.6	59	28	BX289623	BX289623 Arabidops	C 915	10.6	37.9	39	2	HSM010339	HSM010339
38.6	59	29	BX653271	BX653271 Arabidops	916	10.6	37.9	39	28	AZ826153	AZ826153
38.6	59	29	BX662691	BX662691 Arabidops	C 917	10.6	37.9	39	28	AZ946943	AZ946943
38.6	59	29	CNS040FI	AL268839 Tetraodon	918	10.6	37.9	39	29	CC800300	CC800300
38.6	59	29	TA142G08Q	AL466521 T. brucei	C 919	10.6	37.9	39	29	AG256137	AG256137
38.6	59	29	TA232D07P	AL481048 T. brucei	C 920	10.6	37.9	40	9	AA029741	AA029741
38.6	60	9	AA415453	AA415453 vc99b07.s	921	10.6	37.9	40	9	AI014602	AI014602
38.6	60	12	BH793877	BH793877 ie35ell.y	922	10.6	37.9	40	9	AI264704	AI264704
38.6	60	12	BM529568	BM529568 fx46el0.y	923	10.6	37.9	40	14	CA796225	CA796225
38.6	60	12	BM529744	BM529744 fx46e07.y	924	10.6	37.9	40	14	H41025	H41025
38.6	60	12	BM530440	BM530440 fx25g08.y	925	10.6	37.9	40	29	CG869712	CG869712
38.6	60	12	BM530674	BM530674 fx47el0.y	926	10.6	37.9	40	29	BX234325	BX234325
38.6	60	12	BM532766	BM532766 fx46b10.y	C 927	10.6	37.9	40	29	HA247016	HA247016
38.6	60	12	BM533801	BM533801 fx46f01.y	928	10.6	37.9	41	12	B1819153	B1819153
38.6	60	12	BM572474	BM572474 fx28d04.y	929	10.6	37.9	41	14	R76301	R76301
38.6	60	12	BM858725	BM858725 fx78g12.y	930	10.6	37.9	41	28	AZ596544	AZ596544
38.6	60	13	BQ127992	BQ127992 ij79h08.y	C 931	10.6	37.9	41	28	AZ615427	AZ615427
38.6	60	13	BQ128109	BQ128109 ij81g02.y	C 932	10.6	37.9	41	28	AZ848135	AZ848135
38.6	60	13	BQ130809	BQ130809 ij87h10.y	C 933	10.6	37.9	41	28	AZ976999	AZ976999
38.6	60	13	BQ268119	BQ268119 ij95d10.y	934	10.6	37.9	41	29	TA40D01Q	TA40D01Q
38.6	60	13	BQ268123	BQ268123 ij95e07.y	C 935	10.6	37.9	42	13	BX621457	BX621457
38.6	60	13	BQ268195	BQ268195 ij96d12.y	936	10.6	37.9	42	29	CC799723	CC799723
38.6	60	13	BQ631077	BQ631077 ij16a08.y	C 937	10.6	37.9	43	9	AA906764	AA906764
38.6	60	13	BU077819	BU077819 im39e02.y	C 938	10.6	37.9	43	10	BE373472	BE373472
38.6	60	13	BU789770	BU789770 io42a04.y	939	10.6	37.9	43	14	T17570	T17570
38.6	60	13	BU948363	BU948363 io50c01.y	C 940	10.6	37.9	43	29	CG724749	CG724749
38.6	60	14	CD713175	CD713175 VVB187A11	941	10.6	37.9	43	29	BX292057	BX292057
38.6	60	14	CD963363	CD963363 SDU_100 G	942	10.6	37.9	44	28	AZ303870	AZ303870
38.6	60	14	H52868	H52868 EST0022 Tes	C 943	10.6	37.9	44	28	AZ588580	AZ588580
38.6	60	18	AZ921949	AZ921949 HRC021C11	944	10.6	37.9	44	28	AZ603654	AZ603654
38.6	60	28	BH799063	BH799063 1008114A0	C 945	10.6	37.9	45	14	H91384	H91384
38.6	60	28	BZ412803	BZ412803 XA016 Bay	C 946	10.6	37.9	45	28	AZ822654	AZ822654
38.6	60	29	CC883477	CC883477 SALK_0944	C 947	10.6	37.9	45	28	BZ763943	BZ763943
38.6	60	29	TA126E03P	AL463818 T. brucei	C 948	10.6	37.9	46	9	AI131945	AI131945
37.9	19	28	AZ495849	AZ495849 IM0331N22	949	10.6	37.9	46	9	AI188695	AI188695
37.9	20	28	AZ387347	AZ387347 IM0146K12	950	10.6	37.9	46	9	AI300677	AI300677
37.9	23	12	BM399459	BM399459 5009-0-57	951	10.6	37.9	46	9	AI941313	AI941313
37.9	23	12	BM399514	BM399514 5009-0-58	952	10.6	37.9	46	9	AI941313	AI941313
37.9	23	28	AZ849204	AZ849204 2M0150J02	C 953	10.6	37.9	46	9	AA485011	AA485011

37.9 46 10 AW672631
37.9 46 14 R89440
37.9 46 14 T80129
37.9 46 28 A2990941
37.9 47 28 B2764482
37.9 48 9 A1568232
37.9 48 9 AV844988
37.9 48 28 A2452059
37.9 48 28 A2485287
37.9 48 28 B2383007
37.9 49 9 AA902559
37.9 49 12 B1315732
37.9 49 13 BQ101179
37.9 49 13 BQ548140
37.9 49 28 B2767173
37.9 50 9 AU102558
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37.9 53 28 AZ623781
37.9 53 28 BH214712
37.9 53 28 BH902261

AW672631 9A Explan
R89440 YQ05a01.r1
T80129 x017h02.s1
A2990941 2M0274E23
B2764482 SALK_1249
A1568232 tn67d03.x
AV844988 AV844988
A2452059 IM0251P12
A2485287 IM0312D07
B2383007 SALK_1192
AA902559 o159b12.s
B1315732 saf78g09.
BQ101179 i125a03.y
BQ548140 rd20h05.y
B2767173 SALK_1384
AU102558 AU102558
AU104700 AU104700
AU104869 AU104869
AU105640 AU105640
AU105965 AU105965
AU105967 AU105967
AU106392 AU106392
AU106561 AU106561
AZ937712 2M0196E01
BZ352480 SALK_0806
BZ352482 SALK_0806
BZ763937 SALK_1228
BX722118 BX722118
AZ760116 IM0553K04
BH863979 SALK_0950
AL481361 T. brucei
AA856040 vW82a06.x
AA932205 om84g04.s
A1089855 Q20d06.x
AA170022 m84b08.x
AU009185 AU009185
BE321071 NF033E04R
AZ796236 2M0051E21
BH856416 SALK_0797
BZ768008 SALK_1396
AA846708 a14b12.s
AU258826 AU258826
AZ623781 IM0461N17
BH214712 1006004C0
BH902261 SALK_0915

ALIGNMENTS

148819 46 bp mRNA linear EST 14-MAR-2002
148819 Nori Satoh unpublished cDNA library, egg Ciona
estinalis cDNA clone cieg03p13 5', mRNA sequence.
148819
148819.1 GI:19426578

ona intestinalis
ona intestinalis
caryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
lebobranchia; Cionidae; Ciona.
(bases 1 to 46)
on.N., Satou,Y., Kohara,Y. and Shin-i,T.
pressed genes in Ciona intestinalis
published (2000)
tact: Nori Satoh
partment of Zoology
ro University
kyo-Ku, Kyoto, Kyoto 606-8502, Japan
1: 81-75-753-4081

FEATURES
source
1..46
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cieg03p13"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library"

ORIGIN

Query Match 60.7%; Score 17; DB 9; Length 46;
Best Local Similarity 76.9%; Pred. No. 1.5e+04;
Matches 20; Conservative 0; Mismatches 6; Indels 0;

QY 3 CATCATCTCTCGCATGTCAGGTCAAT 28
|||||
DB 33 CATCCCATCGCATGTCAGGTCAAT 8
|||||

RESULT 2
AI762609 49 bp mRNA linear EST
LOCUS AI762609
DEFINITION wi56d08.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:
similar to TR:Q90706 Q90706 CLE7.1; mRNA sequence.
AI762609
ACCESSION AI762609
VERSION AI762609.1 GI:5178276
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM
Homo sapiens
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 49)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Projec
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmer
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequen
Clone distribution: NCI-CGAP clone distribution inform
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert length: 1004 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES source

1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2394255"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/clone_lib="NCI CGAP Col6"
/notes="Organ: colon; Vector: p7713D-Pac (Pharm
modified polylinker; Site 1: Not 1; Site 2: Ec
Plasmid DNA from the normalized library NCI-CC
prepared, and ss circles were made in vitro. f
purification, this DNA was used as tracer in a
hybridization reaction. The driver was PCR-amt
from a pool of 5,000 clones made from the same
(cloneIDs 1057416-1061255, and 114584-114555)
Subtraction by Bento Soares and M. Fatima Bone

ORIGIN

09:04:23 2004

us-10-090-326-23.max.rst

57.1%; Score 16; DB 9; Length 49;
ilarity 79.2%; Pred. No. 3.8e+04;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;
TCATCTCTGCATGTCAGGTC 26
|||||
GCATTATCTGCATATTTCAGGTC 27
55 57 bp mRNA linear EST 18-OCT-1999
061E3R Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
yo Caenorhabditis elegans cDNA clone yk61e3 3', mRNA sequence.
55 55.1 GI:11110762
orhabditis elegans
orhabditis elegans
ryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
dideoa; Rhabditidae; Peloderinae; Caenorhabditis.
bases 1 to 57)
ra,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
ra,H.
rd an expression map of the C.elegans genome
ished (1994)
act: Yuji Kohara
me Biology Lab.
onal Institute of Genetics
1111, Mishima, Shizuoka 411, Japan
81-559-81-6854
81-559-81-6855
1: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .57
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk61e3"
/sex="hermaphrodite"
/dev_stage="embryo"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
56.4%; Score 15.8; DB 14; Length 57;
ilarity 74.1%; Pred. No. 4.8e+04;
Conservative 0; Mismatches 7; Indels 0; Gaps 0;
TCATCTCTGCATGTCAGGTC 27
|||||
TCATCTCTCCACTGTCAGGTC 7
38981 59 bp mRNA linear EST 17-JAN-2003
2_jx10d12.w1 Soares NMBPA Mus musculus cDNA clone IMAGE:5024687
mRNA sequence.
38981
38981.1 GI:27797268
musculus (house mouse)
musculus
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
halia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 59)
CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
ional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
or Gene Index
blished (1997)
Contact: Robert Strauberg, Ph.D.
Email: cgaps@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intram
Sequencing Center (NTSC)
Clone distribution: NCI-CGAP clone distribution informa
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: L1AM11070 row: G column: 24
Seq primer: T7 primer.
Location/Qualifiers
1. .59
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5024687"
/tissue_type="pituitary gland"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares NMBPA"
/note="Organ: brain; Vector: pT7T3D-PacI; Site-
Site 2: EcoRI; 1st strand cDNA was primed with-
oligo(dT) primer
5'-AATCGAAGATTCGCGCGCGTATCATGATTTT
double-stranded cDNA was ligated to EcoRI adapt
5'-AATTCGCGCAGG-3' AND 5'-CTCGTGGCG-3' (Pharm
digested with NotI and cloned into the NotI and
sites of the pT7T3D-PacI vector. Library went t
round of normalization, and was constructed in
laboratory of M. Bento Soares (University of Ic
Query Match 54.3%; Score 15.2; DB 14; Length 59;
Best Local Similarity 71.4%; Pred. No. 8.2e+04;
Matches 20; Conservative 8; Indels 0;
QY 1 AGCATCATCTCTGTCATGTCAGGTCAT 28
|||||
Db 40 AGCAGGTTGCTCTCCTCGTGGTGGGTCCT 13
RESULT 5
AW458816 60 bp mRNA linear EST
LOCUS
DEFINITION
Gm-c1016-4807 5', mRNA sequence.
ACCESSION
AW458816
VERSION
AW458816.1 GI:7029033
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; I
Glycine.
1 (bases 1 to 60)
Shoemaker,R., Keim,E., Vodkin,L., Erpelting,J., Coryell,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., M
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., I
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Car
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108.
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Cor

09:04:23 2004

us-10-090-326-23.max.rst

h Memorial Parkway Huntsville, AL 35801 For further information
: (800)-533-4363 or contact via email: ccu@resgen.com
it Length: 272 Std Error: 0.00
primer: -40RP from Gibco.
Location/Qualifiers

1..60
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl016-4807"
/tissue_type="immature flowers of field grown plants"
/lab_host="Xl10-Gold"
/clone_lib="Gm-cl016"
/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into Xl10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelding."

52.9%; Score 14.8; DB 10; Length 60;
nilarity 73.1%; Pred. No. 1.2e+05;
Conservative 0; Mismatches 7; Indels 0; Gaps 0;

ATCATCCTCTGCATGTCAGTCAT 28
|||||
ATCTACCTATGATGTTAAGTTAT 41

96377 27 bp mRNA linear EST 17-JAN-2002
9-0-21-F09.t.2 Chilcoat/Turkewitz cDNA (large fraction)
rahymena thermophila cDNA, mRNA sequence.

96377 GI:18196550

rahymena thermophila
rahymena thermophila
aryota; Alveolata; Ciliophora; Oligohymenophorea;
tenostomatida; Tetrahymenina; Tetrahymena.
(bases 1 to 27)
kewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
nkel, J. and Klobutcher, L.
from Tetrahymena thermophila, strain CU428.1, growing cells
ublished (2002)
tact: Turkewitz AP
ecular Genetics and Cell Biology
iversity of Chicago
E. 58th Street, Chicago, IL 60637, USA
.: 773 702 4374
t: 773 702 3172
ail: apturkew@midway.uchicago.edu
I primer: T3.
Location/Qualifiers
1..27
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript 2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 52.1%; Score 14.6; DB 12; Length 27;
Best Local Similarity 77.3%; Pred. No. 9.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0;

QY 2 GCATCATCCTCTGCATGTCAG 23
|||
Db 23 GCGACATCCACNCGCTGTCAG 2

RESULT 7
AA515410/c

LOCUS
DEFINITION
AA515410 49 bp mRNA linear EST
nf69a09.s1 NCI CGAP Co3 Homo sapiens cDNA clone IMAGE:9;
similar to TR:G189049 G189049 NADH UBIQUINONE OXIDOREDU
SUBUNIT ; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AA515410
AA515410.1 GI:2255010
Homo sapiens (human)
EST.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 49)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Projec
Tumor Gene Index
Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmer
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequen
Clone distribution: NCI-CGAP clone distribution inform
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1832 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

FEATURES
source

1..49
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:925144"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
/clone_lib="NCI CGAP Co3"
/notes="Vector: p773D-Pac (Pharmacia) with a p
polylinker; Site 1: Not I; Site 2: Eco RI; 1st
was prepared from 12 pooled bulk tumor samples
with a Not I - oligo(dT) primer. Double-stranc
ligated to Eco RI adaptors (Pharmacia), digest
I and cloned into the Not I and Eco RI sites c
modified p773 vector. Library went through or
normalization."

ORIGIN

Query Match 52.1%; Score 14.6; DB 9; Length 49;
Best Local Similarity 81.0%; Pred. No. 1.3e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0;

QY 7 ATCTCTGCATGTCAGTCA 27
|||||
Db 44 ATCTCTGCATGTCAGTCA 24

5838 0_361A18.T7 CHORI-240 DNA linear GSS 17-JUN-2003
 5838 Bos taurus genomic clone CH240_361A18,
 mic survey sequence.
 5838.1 GI:31834126
 taurus (cow)
 taurus
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 alia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 dae; Bovinae; Bos.
 bases 1 to 51
 .R., Clottier, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
 .M., Stott, J., Lee, D., Girm, N., Olson, T., Mayo, M.,
 erfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,
 ewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
 in, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,
 ymple, B.P. and Tellam, R.
 ne BAC End Sequences from Library CHORI-240, PLATES 294 to 398
 ublished (2003)
 pr GSSs: CH240_361A18.TARBAC13P2
 tact: Rob Holt
 tencing
 British Columbia Cancer Agency Genome Science Centre
 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
 : 604-877-6085
 : 604-877-6276
 l: rhoit@bcgsc.ca
 es are derived from the bovine BAC library CHORI-240
 p://www.chori.org/bacpac/bovine240.htm). For BAC library
 ability, please contact Pieter de Jong (pdejong@mail.cho.org).
 es may be purchased from BACPAC Resources
 p://www.chori.org/bacpac/ordering/information.html). This work
 undertaken as part of the International Bovine BAC Mapping
 ortium (IBBMC) by CSIRO Livestock Industries, Australia and the
 ish Columbia Genome Sciences Centre, Canada.
 e: 361 row: A column: 18
 primer: T7
 s: BAC ends.
 Location/Qualifiers
 1..51
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strains="breed: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_361A18"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"
 51.4%; Score 14.4; DB 29; Length 51;
 ilarity 75.0%; Pred. No. 1.5e+05;
 Conservative 0; Mismatches 6; Indels 0;
 CATCATCTCTGCATGCTGAGG 24
 CATCATCTCTGCATGCTGAGG 25
 53116 55 bp DNA linear GSS 13-MAR-2003
 X_113520.16.90.x Arabidopsis thaliana TDNA insertion lines
 idopsis thaliana genomic clone SALK_113520.16.90.x, genomic
 ey sequence.
 53116
 53116.1 GI:28935669

KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tri
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudi
 rosids; eurosids II; Brassicales; Brassicaceae; Arabido
 1 (bases 1 to 55)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H.,
 Shinn, P., Zimmermann, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left bo
 TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1..55
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_113520.16.90.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion
 /note="PCR was performed on Arabidopsis thalian
 each of which contains one or more TDNA inser
 elements. The resultant fragment for each line
 directly sequenced to determine the genomic se
 the site of insertion. Details of the protoc
 be found at http://signal.salk.edu/tdna_protoc
 ORIGIN
 Query Match 51.4%; Score 14.4; DB 28; Length 55;
 Best Local Similarity 75.0%; Pred. No. 1.6e+05;
 Matches 18; Conservative 0; Mismatches 6; Indels 0;
 QY 5 TCATCTCTGCATGCTGAGGTCAT 28
 DB 30 TTATTTCTTCATGCTGAGGACAT 53
 RESULT 10
 AZ591147 36 bp DNA linear GSS
 LOCUS 1M0401D16F Mouse 10kb plasmid UUGC1M library Mus musculi
 DEFINITION clone UUGC1M0401D16 F, genomic survey sequence.
 ACCESSION AZ591147
 VERSION AZ591147.1 GI:11713433
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
 1 (bases 1 to 36)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Har
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen,
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads fr
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030
 84112, USA

801 585 5606
 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0491 row: D column: 16
 Seq primer: CGTTGTAACACGCGCCAGT
 s: plasmid ends
 quality sequence stop: 36.
 Location/Qualifiers

1. .36
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0401D16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

50.7%; Score 14.2; DB 28; Length 36;
 milarity 84.2%; Pred.No. 1.5e+05; Indels 0; Gaps 0;
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCTGTCATGTCAGGTCA 27
 |||||
 TCTGAGGGTCAGGGCA 20

35338 39 bp DNA linear GSS 13-DEC-2000
 491E10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 ne UUGC1M0491E10 R, genomic survey sequence.
 35338
 35338.1 GI:11757528

musculus (house mouse)
 musculus
 alyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (bases 1 to 39)
 n.D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 am.H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 lly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 derhausen,A. and Wright,D., Weiss,R.
 se whole genome scaffolding with paired end reads from 10kb
 smid inserts
 ublished (2000)
 tact: Robert B. Weiss
 versity of Utah Genome Center
 .versity of Utah
 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 .12, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0491 row: E column: 10
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 39.
 Location/Qualifiers

1. .39
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0491E10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA fr
 musculus C57BL/6J (male) was obtained from the
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/
 was hydrodynamically sheared by repeated passag
 0.005 inch orifice at constant velocity. The sh
 was blunt end-repaired with T4 DNA polymerase
 polynucleotide kinase. Adaptor oligonucleotides
 ligated to the blunt ends in high molar excess
 adaptor DNA was purified and size-selected fo
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-num
 inducible derivative of plasmid R1. The vector
 with adaptors complementary to the insert adapt
 purified. The sheared, adaptor mouse DNA was
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Strata
 and selected for ampicillin resistance."

ORIGIN

Query Match 50.7%; Score 14.2; DB 28; Length 39;
 Best Local Similarity 70.4%; Pred.No. 1.6e+05;
 Matches 19; Conservative 0; Mismatches 8; Indels 0;

QY 1 AGCATCATCTCTGCATGTCAGGTCA 27
 |||||
 Db 38 AGCAGCAGCAGCAGCAGGTGAGGCA 12

RESULT 12
 AZ330881

LOCUS
 DEFINITION
 1M0056101R Mouse 10kb plasmid UUGC1M library Mus muscul
 clone UUGC1M0056101 R, genomic survey sequence.

ACCESSION
 AZ330881

VERSION
 AZ330881.1 GI:10393023

KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu

REFERENCE
 1 (bases 1 to 50)

AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Ha
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads fr
 plasmid inserts

JOURNAL
 Unpublished (2000)

COMMENT
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
 84112, USA

```

801 585 5606
801 585 7177
l: dnm@genetics.utah.edu
rt Length: 10000 Std Error: 0.00
e: 0056 row: 1 column: 01
primer: CACACAGGAACAGCATGACC
is: plasmid ends
quality sequence stop: 50.
Location/Qualifiers
1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0056101"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWP42nv; Purified genomic DNA from M. musculus CS7BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
50.7%; Score 14.2; DB 28; Length 50;
ilarity 70.4%; Pred. NO. 1.8e+05;
Conservative 0; Mismatches 8; Indels 0; Gaps 0;
ATCATCTCTGCATGTCATGTCAT 28
|||||
AACACACTCTGCATGTTAGATCT 49

1765 58 bp mRNA linear EST 20-NOV-2003
1765 XGC-gastrula silurana tropicalis cDNA clone TGas036n10 5',
sequence.
1765
1765.1 GI:17662001

rana tropicalis (western clawed frog)
rana tropicalis
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
podinae; Silurana.
(bases 1 to 58)
ing,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
fer Xenopus tropicalis EST project 2001 (11_2003)
blished (2003)
:act: Huckle E
per Institute
ton, Cambridgeshire, CB10 1SA, UK
l: trop@sanger.ac.uk
sequence is from a Xenopus Gene Collection (XGC) library
structed by Aaron M. Zorn.
was oligo dt primed from 5ug of poly A+ RNA from stages 10-13
:ulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with

```

```

EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XLI-blue
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TGas036n10.plkSP6
Sequencing primer: SP6
Location/Qualifiers
1..58
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TGas036n10"
/dev_host="Gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XLI-blue"
/clone_lib="XGC-gastrula"
/note="Vector: pCS107; Site 1: EcoRI; Site 2:
10-13 gastrulae. EcoRI-NotI cut cDNA was then
into pCS107 with EcoRI at the 5' end and NotI
end."
FEATURES
source
1..58
Query Match 50.7%; Score 14.2; DB 9; Length 58;
Best Local Similarity 84.2%; Pred. NO. 1.9e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0;
QY 1 AGCATCATCTCTGCATGG 19
|||||
Db 49 AGCGCATCTCTTCATGG 31
|||||

RESULT 14
GGA320139/c 58 bp DNA linear GSS
LOCUS
Gallus gallus anonymous sequence from Cosmid mapping to
DEFINITION
microchromosome (Cosmid 32 - Contig 41), genomic survey
ACCESSION
AJ232043
VERSION
AJ232043.1 GI:3451861
KEYWORDS
GSS; genome survey sequence.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 58)
AUTHORS
Morris,J., Bruley,C.K., Paton,I.R., Dunn,I., Jones,C.T.,
Morris,J., Bruley,C.K., Paton,I.R., Dunn,I., Jones,C.T.,
Paton,I.R., Law,A.S., Masabanda,J., Sazanov,A., Waddi;
Pries,R. and Burt,D.W.
Differences in gene density on chicken macrochromosomes
microchromosomes
Anim. Genet. 31 (2), 96-103 (2000)
JOURNAL
MEDLINE
20244064
PUBMED
10782207
REFERENCE
2 (bases 1 to 58)
AUTHORS
Smith,J., Bruley,C.K., Paton,I.R., Law,A.S., Masabanda,J.
Waddington,D., Pries,R. and Burt,D.W.
Direct Submission
TITLE
Submitted (12-AUG-1998) Division of Molecular Biology, F
Institute, Roslin, Midlothian EH25 9PS, Scotland, UK
FEATURES
source
1..58
/organism="Gallus gallus"
/mol_type="genomic DNA"
/db_xref="taxon:9031"
/chromosome="microchromosome"
ORIGIN
Query Match 50.7%; Score 14.2; DB 29; Length 58;
Best Local Similarity 84.2%; Pred. NO. 1.9e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0;
QY 1 AGCATCATCTCTGCATGG 19
|||||

```

3CACAACTCTGCATGG 1

89521 52 bp mRNA linear EST 11-AUG-1997
 lhl2.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone
 GE:843431 5' similar to SW:SPCN_CHICK P07751 SPECTRIN ALPHA
 IN, BRAIN ; mRNA sequence.

89521 89521

89521.1 GI:2219123

o sapiens (human)

o sapiens
 aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (bases 1 to 52)
 ller.L., Allen.M., Bowles.L., Dubuque.T., Geisel.G., Jost.S.,
 aba.T., Lacy.M., Le.N., Lennon.G., Marra.M., Martin.J.,
 re.B., Schellenberg.K., Steptoe.M., Tan.F., Theising.B.,
 te.Y., Wylie.T., Waterston.R. and Wilson.R.
 hu-Merck EST Project 1997
 ublished (1997)

tact: Willson RK
 hington University School of Medicine
 4 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 : 314 286 1800
 : 314 286 1810

il: est@watson.wustl.edu
 s clone is available royalty-free through LLNL ; contact the
 GE Consortium (info@image.llnl.gov) for further information.
 ce considered overall poor quality
 sable reversed clone: similarity on wrong strand
 Primer: -28ml3 rev1 ET from Amersham
 h quality sequence stop: 1.
 Location/Qualifiers

1. .52
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:843431"
 /sex="female"
 /dev_stage="HeLa S3 cell line"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene HeLa cell s3 937216"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3
 epitheloid carcinoma cells grown to semi-confluency
 without induction. Average insert size: 1.5 kb; Uni-ZAP XR
 Vector. -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'
 adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

50.0%; Score 14; DB 9; Length 52;
 milarity 100.0%; Pred.No. 2.2e+05;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATGGTCAGGTTCAT 28

|||||

ATGGTCAGGTTCAT 30

92773 52 bp mRNA linear EST 25-JUN-1997
 '609.r1 Stratagene mouse testis (#937308) Mus musculus cDNA
 ne IMAGE:918209 5' similar to SW:12A6 RAT P38062 INITIATION
 TOR 2 ASSOCIATED 67 KD GLYCOPROTEIN ; mRNA sequence.

92773 92773

92773.1 GI:2222335

; musculus (house mouse)

; musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
 1 (bases 1 to 52)

REFERENCE

AUTHORS

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moor
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R.
 Waterston,R.

The WashU-HHMI Mouse EST Project

TITLE

JOURNAL

COMMENT

Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; con
 IMAGE Consortium (info@image.llnl.gov) for further info
 MGI:530425

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev1 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1. .52
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:918209"
 /sex="males"
 /tissue_type="testis"
 /dev_stage="10-12 week old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse testis (#937308)"
 /note="Organ: testis; Vector: pBluescript SK-;
 EcoRI; Site 2: XhoI; cloned unidirectionally.
 Oligo dT. Average insert size: 1.0 kb; Uni-ZAP
 -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match 50.0%; Score 14; DB 9; Length 52;
 Best Local Similarity 77.3%; Pred.No. 2.2e+05;
 Matches 17; Conservative 0; Mismatches 5; Indels 0;

Qy 1 AGCATCATCTCTGCATGGTCA 22

|||||

Db 25 AGCATCACCATCTCCATCTCA 4

RESULT 17

AZ922240

LOCUS

DEFINITION

AZ922240 53 bp DNA linear GSS
 MRCor3C12 Sorghum bicolor MRCor Sorghum bicolor genomic
 Gene for TWP-2-like protein (retrotransposon), genomic
 sequence.

AZ922240

VERSION

KEYWORDS

SOURCE

ORGANISM

Sorghum bicolor (sorghum)
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poace
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

AUTHORS

Peterson,D.G., Schulze,S.R., Sciara,E.B., Lee,S.A., Bow
 Nagel,A., Jiang,N., Tibbitts,D.C., Wessler,S.R. and Pat
 Integration of Cot analysis, DNA cloning, and high-thro
 sequencing facilitates genome characterization and gene
 Genome Res. 12 (5), 795-807 (2002)

21992826

MEDLINE

97346
 tact: Peterson DG
 at Genome Mapping Laboratory
 versity of Georgia
 n 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA
 02, USA
 : 706-583-0167
 : 706-583-0160
 il: dgpearches.uga.edu
 ss: Hydroxyapatite-fractionated DNA.
 Location/Qualifiers
 1..53
 /organism="Sorghum bicolor"
 /mol_type="genomic DNA"
 /cultivar="BTx623"
 /db_xref="taxon:4558"
 /tissue_type="leaves"
 /dev_stage="seedling"
 /clone_lib="Sorghum bicolor MRCot"
 /notes="Vector: pGEN-TA-Easy; A Cot analysis was performed
 for the sorghum genome. Based on the resulting Cot curve,
 hydroxyapatite chromatography was used to isolate
 'highly-repetitive' (HR), 'moderately-repetitive' (MR),
 and 'single/low-copy' (SL) sequence components from
 sheared genomic DNA. The three repetition-based DNA
 components were cloned into E. coli to produce HRCot,
 MRCot, and SLCot genomic libraries. Blotting and
 sequencing data indicates that each library is
 representative of the component from which it was derived.
 Putative ID listings given for sequences are based on
 comparison (blastn) with sequences in the NCBI Nr
 Database. Only the primary match is given (all primary E
 values are < or = 1.00E-5). In no instance does a 'Cot
 clone' contain the complete sequence of its putative Nr
 match."

50.0%; Score 14; DB 28; Length 53;
 alarity 77.3%; Pred. No. 2.2e+05;
 Conservative 0; Mismatches 5; Indels 0;
 Gaps 0;

ATCATCTCTGCATGTCAGG 24
 |||||
 TTATCTCTCAACATCGCCAGG 39

7030D12 56 bp DNA linear GSS 20-JUN-2003
 shmania braziliensis GSS, clone LBAF030D12, genomic survey
 lence.
 12120
 12120.1 GI:32136620
 : Genomic survey sequence.
 shmania braziliensis
 shmania braziliensis
 tryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 shmania; Leishmania braziliensis species complex.
 centino, E.C., Ruiz, J.C. and Cruz, A.K.
 analysis of the Leishmania braziliensis genome
 blished
 (bases 1 to 56)
 z, A.K.
 act Submission
 nitted (17-JUN-2003) Cruz A.K., University of Sao Paulo,
 artment of Molecular and Cell Biology, FMRP, Avenida
 leirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL
 ne requests: akcruz@mrp.usp.br.
 Location/Qualifiers
 1..56
 /organism="Leishmania braziliensis"
 /mol_type="genomic DNA"

ORIGIN

Query Match 50.0%; Score 14; DB 29; Length 56;
 Best Local Similarity 77.3%; Pred. No. 2.3e+05;
 Matches 17; Conservative 0; Mismatches 5; Indels 0;

QY 7 ATCTCTGTCATGTCAGGTCA 28
 |||||
 |||||

Db 2 ATCCCTGCACCGTCAGATGAT 23
 |||||
 |||||

RESULT 19

AUI06538/c

LOCUS

AUI06538

DEFINITION

ADSJ01742, mRNA sequence.

ACCESSION

AUI06538

VERSION

AUI06538.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 50)

AUTHORS

Suzuki, Y., Tsunoda, T., Mizushima-Sugano, J., S.

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Ok

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, la

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

PUBMED

11375929

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: shuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gen

149-156 (1997).

FEATURES

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="ADSJ01742"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 49.3%; Score 13.8; DB 9; Length 50;

Best Local Similarity 72.0%; Pred. No. 2.5e+05;

Matches 18; Conservative 0; Mismatches 7; Indels 0;

QY 3 CATCATCTCTGTCAGGTCA 27
 |||||
 |||||

Db 36 CACGATGATCTGCATTGCAAGTGA 12
 |||||
 |||||

RESULT 20

CB260365/c

LOCUS

CB260365

DEFINITION

52-E9600-013-003-G13-t7r MP1Z-ADIS-013 Arabidopsis thal:

clone MP1Zp770G13Q 5-PRIME, mRNA sequence..

CB260365

VERSION

CB260365.1

KEYWORDS

EST.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tri

tmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 (bases 1 to 51)
 nid.K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
 chelli-Olds,T. and Weisshaar,B.
 ge-scale identification and analysis of genome-wide
 gie-nucleotide polymorphisms for mapping in Arabidopsis thaliana
 one Res. 13 (6), 1250-1257 (2003)

83290

99357

tact: Weisshaar B

S DNA core facility at MPZ

-Planck-Institute for Plant Breeding Research

1-von-Linne Weg 10, 50829 Koeln, Germany

il: 00492215062851

il: weisshaar@mpiz-koeln.mpg.de

ert Length: 51 Std Error: 0.00

te: 3 row: G column: 13

Primer: T7R: CTAATACGACTCACTATAGGGA.

Location/Qualifiers

1. 51

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/cultivar="Niederzents-1 (Nd-1)"

/db_xref="GABI:588847"

/db_xref="taxon:3702"

/clone="MPZP770G133Q"

/tissue_type="whole plant"

/dev_stage="adult plant, mixed stresses"

/lab_host="E. coli TOP10"

/clone_lib="MPZ-ADIS-013"

/note="vector: pSPOR11; Site 1: Sali; Site 2: NotI; RNA
 from total, adult, 6 weeks old Arabidopsis thaliana
 (accession Nd-1) plants, grown in the greenhouse under
 long day conditions in soil treated for 24 hours with
 different stresses. (1) at 4 Grad C in the dark, (2) at
 37 Grad C in the dark, (3) lying in the lab after removing
 from soil, (4) in the greenhouse after wounding with a
 forceps, (5) in the lab watering with a 150 mM NaCl
 solution, (6) at 26 Grad C in the light/UV; equal
 quantities of stressed plant material were pooled; library
 was made at the Max-Planck-Institute for Plant Breeding
 Research, Cologne, Germany; cloning sites Sali-NotI,
 primer sites and orientation:
 T7-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-NotI-SP6; Note:
 Sequencing granted in the context of the GABI Arabidopsis
 Verbund I: Genetic Diversity, 'Establishment of
 high-efficiency SNP-based mapping tools and development of
 methods for genome-wide mutation detection'. PI: Bernd
 Weisshaar Sequence submission managed by RZPD/GABI-Primary
 database: <http://gabi.rzpd.de>. This clone is available
 from RZPD; contact RZPD (clone@rzpd.de) for further
 information."

49.3%; Score 13.8; DB 14; Length 51;

milarity 72.0%; Pred.No. 2.6e+05;

Conservative 0; Mismatches 7; Indels 0; Gaps 0;

GCATCATCCCTCGTCAGTCAAGT 25

GGAGCATCGTTTCGTGTCAGT 20

'89849

'03BH01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ne UUGC2M003BH01 F, genomic survey sequence.

'89849

'89849.1 GI:12931098

; musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
 1 (bases 1 to 55)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Ha
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads fr

TITLE

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: rdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0038 row: H column: 01

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 55.

FEATURES

source

1. 55

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M003BH01"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resist
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA f
 musculus C57BL/6J (male) was obtained from th
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares>
 was hydrodynamically sheared by repeated passa
 0.005 inch orifice at constant velocity. The s
 was blunt end-repaired with T4 DNA polymerase
 polynucleotide kinase. Adaptor oligonucleotide
 ligated to the blunt ends in high molar exces
 adapted DNA was purified and size-selected f
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-nu
 inducible derivative of plasmid R1. The vector
 with adaptors complementary to the insert adap
 purified. The sheared, adapted mouse DNA was
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Strata
 and selected for ampicillin resistance."

ORIGIN

Query Match 49.3%; Score 13.8; DB 28; Length 55;

Best Local Similarity 72.0%; Pred. No. 2.7e+05;

Matches 18; Conservative 0; Mismatches 7; Indels 0;

QY 3 CATCATCCCTCGTCAGTCAAGTCA 27

Db 37 CTTCATCCCTCGTTTGCACACTTA 13

RESULT 22

BH911716/c

LOCUS

BH911716 57 bp DNA linear GSS

DEFINITION

SALK_071735.19.20.x Arabidopsis thaliana TDNA insertion

Arabidopsis thaliana genomic clone SALK_071735.19.20.x,

survey sequence.

ACCESSION

BH911716

VERSION

BH911716.1 GI:22724649

KEYWORDS

GSS.

oidopsis thaliana (thale cress)
 cidopsis thaliana
 arnata; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 rmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 ids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
 (bases 1 to 57)
 nso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 rinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 nm,P., Zimmerman,J. and Ecker,J.R.
 sequence-indexed Library of Insertion Mutations in the
 bidopsis Genome
 ublished (2001)
 tact: Joseph R. Ecker
 k Institute Genomic Analysis Laboratory (SIGnAL)
 Salk Institute for Biological Studies
 10 N. Torrey Pines Road, La Jolla, CA 92037, USA
 : 858 453 4100 x1752
 : 858 558 6379
 il: ecker@salk.edu
 s is single pass sequence recovered from the left border of
 A. This sequence lies within 300 bases of the 3' end of
 944560.
 ss: TDNA tagged.

Location/Qualifiers
 1. .57
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK 071735.19.20.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html

49.3%; Score 13.8; DB 28; Length 57;
 milarity 72.0%; Pred. No. 2.7e+05;
 Conservative 0; Mismatches 7; Indels 0; Gaps 0;

TATCCTCTGCATGTCAGGTGTCAT 28
 |||||
 TTATTTCTACATGATTAGATCAT 18

69799 59 bp mRNA linear GSS 26-NOV-2003
 931 Sanger Institute Gene Trap Library pGT01xf Mus musculus
 A, mRNA sequence.
 69799
 69799.1 GI:38533479

musculus (house mouse)
 musculus
 aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (bases 1 to 59)
 ger Intitute Gene Trap Resource.
 p://www.sanger.ac.uk/PostGenomics/genetrap/
 ublished (2003)
 tact: Sanger Institute Gene Trap Resource
 lcome Trust Sanger Institute
 il: info.genetrap@sanger.ac.uk
 uence tag generated by 5' RACE of total RNA from gene trap ES
 l line. ES cell lines harboring insertion mutation of target
 e are available upon request from Sanger Institute Gene Trap
 ource. Annotation information available from
 p://www.sanger.ac.uk/PostGenomics/genetrap/
 ss: Gene Trap.

FEATURES

source
 1. .59
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129 OLA"
 /db_xref="taxon:10090"
 /sex="Male"
 /cell_type="Embryonic Stem Cell"
 /clone_lib="Sanger Institute Gene Trap Library"
 /note="Vector: pGT01xf"

ORIGIN

Query Match 49.3%; Score 13.8; DB 29; Length 59;
 Best Local Similarity 72.0%; Pred. No. 2.7e+05;
 Matches 18; Conservative 0; Mismatches 7; Indels 0;

QY 2 GCATCATCTCTGCATGTCAGGTC 26
 |||||

Db 49 GCATCATCTATAATATGTCAGTC 25
 |||||

RESULT 24
 AZ824496/c
 LOCUS 37 bp DNA linear GSS
 DEFINITION 2M0099C12F Mouse 10kb plasmid UUGC1M library Mus muscul
 clone UUGC2M0099C12 F, genomic survey sequence.
 ACCESSION AZ824496
 VERSION AZ824496.1 GI:12994404
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
 1 (bases 1 to 37)

REFERENCE
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Ha
 Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,
 Reilly,M., Rose,M., Rose,R., Stokes,R., finge,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads fr
 plasmid inserts
 Unpublished (2000)

TITLE Contact: Robert B. Weiss
 JOURNAL University of Utah Genome Center
 COMMENT University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 203C
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0099 row: C column: 12
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 37.

FEATURES

source
 1. .37
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0099C12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resist
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA f
 musculus C57BL/6J (male) was obtained from th
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares
 was hydrodynamically sheared by repeated passa
 0.005 inch orifice at constant velocity. The s
 was blunt end-repaired with T4 DNA polymerase
 polynucleotide kinase. Adaptor oligonucleotide
 ligated to the blunt ends in high molar exces

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

48.6%; Score 13.6; DB 28; Length 37;
 nilarity 80.0%; Pred. No. 2.6e+05;
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 SCATCATCTCTGCATGGT 20
 |||||
 SCACCTCCCTTCATGGT 1

26656 46 bp DNA linear GSS 15-SEP-2003
 0614-06A1-B06 UniformMu MutAIL Library Zea mays genomic clone
 0614-06A1-B06, genomic survey sequence.
 26656
 26656.1 GI:34735136

mays
 may
 aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 rmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 de; Panicoideae; Andropogoneae; Zea.
 (bases 1 to 46)
 Shaw S., Tan B.-C., Settles A.M. and McCarty D.R.
 uence tagged transposon insertions from the UniformMu maize
 ulation
 ublished (2003)
 tact: Donald R. McCarty
 nt Molecular and Cellular Biology Program
 versity of Florida
 110690 Gainesville, FL 32611-0690, USA
 : 352-392-1928 x322
 il: drmc@ufl.edu
 uence flanking probable Mu insertion site in UniformMu line:
 0614-06, primer set: A
 ss: transposon insertion site.
 Location/Qualifiers
 1..46
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="W22 (ACR, bz1-m9)"
 /cultivar="UniformMu"
 /db_xref="taxon:4577"
 /clone_lib="UniformMu MutAIL Library"
 /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
 insertions in Mu inactive lines were extracted from the
 UniformMu maize population by the thermo asymmetric
 interlaced PCR (TAIL) protocol using primers specific for
 the Mu terminal inverted repeat and a set of 16 arbitrary
 primers. Amplicons were size enriched using Sepharose 400
 spin columns and cloned into the TOPO PCR4 vector."

48.6%; Score 13.6; DB 29; Length 46;
 imilarity 67.9%; Pred. No. 2.9e+05;
 : Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 AGCATCATCTCTGCATGGTCATGTCAT 28
 |||||
 AGCAGCATCAAAAGCTTAGTGAGGTGAT 18

RESULT 26
 AI670113/c
 LOCUS
 DEFINITION

AI670113 49 bp mRNA linear EST
 wc11h10.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:
 similar to TR:Q61402 Q61402 GRANULE CELL ANTISERUM POSI
 mRNA sequence.

ACCESSION
 VERSION
 AI670113.1 GI:4834887
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens

REFERENCE
 1 (bases 1 to 49)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Projec
 Tumor Gene Index

UNPUBLISHED (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D.,
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Sequencing by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequen
 Clone distribution: NCI-CGAP clone distribution inform
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1..
 Location/Qualifiers
 1..49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2314915"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Pr28"
 /note="Organ: prostate; Vector: pT7T3D-Pac (Ph
 with a modified polylinker; Plasmid DNA from c
 normalized library NCI CGAP Pr22 was prepared,
 circles were made in vitro. Following HAP puri
 this DNA was used as tracer in a subtractive h
 reaction. The driver was PCR-amplified cDNAs f
 of 5,000 clones made from the same library (cl
 985608-986759, 1101192-1101959, and 1217928-12
 Subtraction by Bento Soares and M. Fatima Bona

FEATURES
 source

Query Match 48.6%; Score 13.6; DB 9; Length 49;
 Best Local Similarity 76.2%; Pred. No. 3e+05; Indels 0;
 Matches 16; Conservative 0; Mismatches 5;
 QY 5 TCATCTCTCTGCATGGTCAGGT 25
 |||||
 Db 49 TCATCATATGCATGTCAGGT 29
 |||||

ORIGIN

Query Match 48.6%; Score 13.6; DB 9; Length 49;
 Best Local Similarity 76.2%; Pred. No. 3e+05; Indels 0;
 Matches 16; Conservative 0; Mismatches 5;
 QY 5 TCATCTCTCTGCATGGTCAGGT 25
 |||||
 Db 49 TCATCATATGCATGTCAGGT 29
 |||||

RESULT 27
 BQ086305/c

LOCUS
 DEFINITION
 i121302.y1 Melton Normalized Human Islet 4 N4-HIS 1 Hom
 cDNA clone IMAGE:6135075 5', mRNA sequence.
 ACCESSION
 BQ086305
 VERSION
 BQ086305.1 GI:20045509
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)

ORGANISM	Arabidopsis thaliana	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr	
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudi rosids; eurosids II; Brassicales; Brassicaceae; Arabido	
	1 (bases 1 to 53)	
	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Shinn,P., Zimmerman,J. and Ecker,J.R.	
TITLE	A Sequence-Indexed Library of Insertion Mutations in th	
JOURNAL	Arabidopsis Genome	
COMMENT	Unpublished (2001)	
	Contact: Joseph R. Ecker	
	Salk Institute Genomic Analysis Laboratory (SIGNAL)	
	The Salk Institute for Biological Studies	
	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA	
	Tel.: 858 453 4100 x1752	
	Fax: 858 558 6379	
	Email: ecker@salk.edu	
	This is single pass sequence recovered from the left bo	
	TDNA. This sequence lies within an annotated exon of At	
	Class: TDNA tagged.	
FEATURES	Location/Qualifiers	
source	1..53	
	/organism="Arabidopsis thaliana"	
	/mol_type="genomic DNA"	
	/strain="Columbia 0"	
	/db_xref="taxon:3702"	
	/clone="SALK_025297.38.35.x"	
	/clone_lib="Arabidopsis thaliana TDNA insertio	
	/note="PCR was performed on Arabidopsis thalia	
	each of which contains one or more TDNA inser	
	elements. The resultant fragment for each lin	
	directly sequenced to determine the genomic se	
	the site of insertion. Details of the proto	
	be found at http://signal.salk.edu/tdna_proto	
ORIGIN		
Query Match	48.6%; Score 13.6; DB 28; Length 53.	
Best Local Similarity	67.9%; Pred. No. 3.le+05;	
Matches	19; Conservative 0; Mismatches 9; Indels 0;	
QY	1 AGCATCATCTCTGCGATGGTCAGGTCAT 28	
dbb	29 AGCAACAACCTTTGATTTGTCAGCTTT 2	
RESULT 29	53 bp DNA linear GSS	
BZ661823/c	SALK_025300.44.70.x Arabidopsis thaliana TDNA insertion	
LOCUS	Arabidopsis thaliana genomic clone SALK_025300.44.70.x,	
DEFINITION	survey sequence.	
ACCESSION	BZ661823	
VERSION	BZ661823.1 GI:28174982	
KEYWORDS	GSS.	
RESOURCE	Arabidopsis thaliana (thale cress)	
ORGANISM	Arabidopsis thaliana	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr	
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudi	
	rosids; eurosids II; Brassicales; Brassicaceae; Arabido	
REFERENCE	1 (bases 1 to 53)	
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Shinn,P., Zimmerman,J. and Ecker,J.R.	
	A Sequence-Indexed Library of Insertion Mutations in th	
TITLE	Arabidopsis Genome	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: Joseph R. Ecker	
	Salk Institute Genomic Analysis Laboratory (SIGNAL)	
	The Salk Institute for Biological Studies	
	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA	
	Tel.: 858 453 4100 x1752	
	Fax: 858 558 6379	

l: eckersalk.edu
is single pass sequence recovered from the left border of
. This sequence lies within an annotated exon of At2g16250.
s: TDNA tagged.
Location/Qualifiers
1. .53
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK 025300.44.70.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

48.6%; Score 13.6; DB 28; Length 53;
ularity 67.9%; Pred. No. 3.1e+05;
Conservative 9; Mismatches 9; Indels 0; Gaps 0;

CATCATCTCTGTCATGGTCAT 28
|||||
CACAAACCTTTGATTGTCTCAGTCT 2

17728 57 bp mRNA linear EST 06-FEB-2003
rbo4f04.y1 COGENE 6E MAN Homo sapiens cDNA clone IMAGE:5795095
mRNA sequence.
17728
17728.1 GI:28265920
s sapiens (human)
s sapiens
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
nalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 57)
-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
tional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
r Gene Index
blished (1997)
tact: Robert Strausberg, Ph.D.
il: cgapsb@mail.nih.gov
A Library Prepared by: The I.M.A.G.E. Consortium/LLNL
NA Library Arrayed by: National Institutes of Health Intramural
A Sequencing Center (NISC)
encing Center (NISC)
one distribution: NCI-CGAP clone distribution information can be
nd through the I.M.A.G.E. Consortium/LLNL at:
oimage.llnl.gov
te: LUAM12897 row: L column: 8
rimer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1. .57
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5795095"
/tissue type="mandible, pooled"
/dev stage="embryo, 6 weeks postconception"
/lab_host="DH10B"
/clone_lib="COGENE 6E MAN"
/note="Vector: pAMP1; cDNA primed using oligo-dT primer,
directionally cloned into UDG sites of pAMP1. Size
selected for insert sizes ranging from 0.2-2.0 kb.
Normalized to Cot5. Primary library, non-amplified.
Library constructed by M. Lovett. For more information on
this library, please contact R. Tidwell (Washington

University) or visit the COGENE website at
<http://hg.wustl.edu/COGENE/>."

ORIGIN
Query Match 48.6%; Score 13.6; DB 14; Length 57;
Best Local Similarity 80.0%; Pred. No. 3.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 3 CATCATCTCTGTCATGGTCAT 22
|||||
1 CATCATCATCATCATCA 20

Db
1 CATCATCATCATCATCA 20

RESULT 31
AI952050/c
LOCUS
DEFINITION
AI952050 58 bp mRNA linear EST
wx45c12.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2
similar to SW:NP11 HUMAN P55209 NUCLEOSOME ASSEMBLY PRO
1. mRNA sequence.

ACCESSION AI952050
VERSION AI952050.1 GI:5744360
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hor
1 (bases 1 to 58)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Pra
I.M.A.G.E. Consortium DNA Sequencing by: Washington Uni
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution inform
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1521 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .58
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2546710"
/tissue type="two pooled squamous cell carcino
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu28"
/note="Organ: lung; Vector: pCMV-SPORT6; Site
Site 2: NotI; Cloned unidirectionally. Primer
Library constructed by Life Technologies."

FEATURES
source
1. .58
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2546710"
/tissue type="two pooled squamous cell carcino
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu28"
/note="Organ: lung; Vector: pCMV-SPORT6; Site
Site 2: NotI; Cloned unidirectionally. Primer
Library constructed by Life Technologies."

ORIGIN
Query Match 48.6%; Score 13.6; DB 9; Length 58;
Best Local Similarity 67.9%; Pred. No. 3.2e+05;
Matches 19; Conservative 0; Mismatches 9; Indels 0;

QY 1 AGCATCATCTCTGTCATGGTCAT 28
|||||
39 ATCCTTCTTCTCTAGATGGACATCAT 12

Db
1 AGCATCATCTCTGTCATGGTCAT 28
39 ATCCTTCTTCTCTAGATGGACATCAT 12

RESULT 32
CA337713
LOCUS
DEFINITION
CA337713 58 bp mRNA linear EST
NISC lw05c10.y1 COGENE 4PA1 Homo sapiens cDNA clone IMA
5', mRNA sequence.
CA337713
ACCESSION

```

17713.1 GI:24555911
> sapiens (human)
> sapiens
> ariyoda; Chordata; Craniata; Vertebrata; Euteleostomi;
> malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 58)
-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
ional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
or Gene Index
blished (1997)
tact: Robert Strausberg, Ph.D.
il: cgaps-remail.nih.gov
A Library Preparation:
NA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
A Sequencing by: National Institutes of Health Intramural
encing Center (NISC)
one distribution: NCI-CGAP clone distribution information can be
nd through the I.M.A.G.E. Consortium/LLNL at:
oeimage.llnl.gov
te: L1AM12414 row: E column: 19
primer: M13Rpl reverse primer (ABI).
Location/Qualifiers
1..58
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cloned="IMAGE:5609466"
/tissue_type="1st pharyngeal arch (pooled)"
/dev_stage="embryo, 4 weeks postconception"
/lab_host="DH10B"
/clone_lib="COGENE 4PAL"
/notes="vector: pAMP1; cDNA primed using oligo-dT primer,
directionally cloned into UDG sites of pAMP1. Size
selected for insert sizes ranging from 0.2-1.2 kb.
Normalized to Col10. Primary library, non-amplified.
Library constructed by M. Lovett. For more information on
this library, please contact R. Tidwell (Washington
University) or visit the COGENE website at
http://hg.wustl.edu/COGENE/."
48.6%; Score 13.6; DB 14; Length 58;
milarity 80.0%; Pred. No. 3.2e+05;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;
ATCATCCTCGCATGTCA 22
|||||
ATCATCATCATCATGTCA 20

142268 59 bp mRNA linear EST 30-OCT-2003
H019XB01f USDA-IPAFS:Expression of Phytophthora sojae genes
ing infection and propagation_sHB Phytophthora sojae cDNA clone
3019B01 5, mRNA sequence.
142268
142268.1 GI:38057922
Phytophthora sojae
Phytophthora sojae
karyota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
(bases 1 to 59)
ler,B.
ler,B. Not Published
ublished (2003)
ntact: Tyler B
ler lab
I
90 Pratt Dr., Blacksburg, VA 24061, USA
1: 540-231-7318

```

```

Email: bmtyleer@vt.edu
PCR Primers
FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 019 row: B column: 01
Seq primer: BK reverse primer
High quality sequence stop: 59.
Location/Qualifiers
1..59
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/cloned="sHB019B01"
/tissue_type="mycelium"
/cell_line="P6497"
/dev_stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone_lib="USDA-IPAFS:Expression of Phytophth
genes during infection and propagation_sHB"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2:
48.6%; Score 13.6; DB 14; Length 59;
Query Match
Best Local Similarity 80.0%; Pred. No. 3.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0;
QY 2 GCATCATCTCTGCATGTTC 21
|||||
DB 38 GCATCATGTCTGCATGGAC 57
|||||

RESULT 34
CD956570/c
LOCUS
DEFINITION SCE 127 GeneTag2 Zea mays cDNA, mRNA sequence.
ACCESSION CD956570
VERSION CD956570.1 GI:32804334
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poace
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 60)
Genoplane.
Genoplane, a major partnership french program in plant
Unpublished (2003)
Contact: Genoplane
Genoplane
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of tl
plant genomics programme 'Genoplane' (http://www.genop
and http://genoplane-info.infobiogen.fr).
Location/Qualifiers
1..60
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="mixture"
/db_xref="taxon:4577"
/clone_lib="GeneTag2"

FEATURES
source
Query Match 48.6%; Score 13.6; DB 14; Length 60;
Best Local Similarity 80.0%; Pred. No. 3.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0
QY 3 CATCATCTCTGCATGTTC 22
|||||
DB 37 CGTCTCTCTTCAAGGTCA 18
|||||

ORIGIN
Query Match 48.6%; Score 13.6; DB 14; Length 60;
Best Local Similarity 80.0%; Pred. No. 3.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0
QY 3 CATCATCTCTGCATGTTC 22
|||||
DB 37 CGTCTCTCTTCAAGGTCA 18
|||||

```

56409 30 bp DNA linear GSS 04-OCT-2000
259F23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ne UUGC1M0259F23 F, genomic survey sequence.

56409 GI:10614630

musculus (house mouse)
musculus
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 30)
n.D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
am,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
lly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
derhausen,A. and Wright,D., Weiss,R.
se whole genome scaffolding with paired end reads from 10kb
smid inserts
ublished (2000)
tact: Robert B. Weiss
versity of Utah Genome Center
versity of Utah
308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
12, USA

: 801 585 5606
: 801 585 7177
il: ddunn@genetics.utah.edu
ert Length: 10000 Std Error: 0.00
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ss: plasmid ends
h quality sequence stop: 30.

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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Similarity 47.9%; Score 13.4; DB 28; Length 30;
Conservative 93.3%; Pred. No. 2.8e+05;
; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3CATGCTCAGGTCAT 28
|||||||
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RESULT 36
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LOCUS

DEFINITION
Arabidopsis thaliana genomic clone SALK_109419.40.15.x,
survey sequence.

ACCESSION
BH906192
VERSION
BH906192.1 GI:22719125
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi
rosids; eurosids II; Brassicales; Brassicaceae; Arabid
1 (bases 1 to 31)

REFERENCE
AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in th
Arabidopsis Genome
Unpublished (2001)

JOURNAL
COMMENT

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left bc
TDNA. This sequence lies within an annotated exon of At
Class: TDNA tagged.

FEATURES
source

Location/Qualifiers
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/clone_lib="Arabidopsis thaliana TDNA insertic
/note="PCR was performed on Arabidopsis thalia
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elements. The resultant fragment for each lin
directly sequenced to determine the genomic se
the site of insertion. Details of the protoc
be found at http://signal.salk.edu/tdna_prot

ORIGIN

Query Match 47.9%; Score 13.4; DB 28; Length 31;
Best Local Similarity 73.9%; Pred. No. 2.9e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0;

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Db 23 CATCATCACCTGCATGTCAGGT 1

RESULT 37
BH906199/c
LOCUS

DEFINITION
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Arabidopsis thaliana genomic clone SALK_109437.33.00.x,
survey sequence.

ACCESSION
BH906199
VERSION
BH906199.1 GI:22719132
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi
rosids; eurosids II; Brassicales; Brassicaceae; Arabid
1 (bases 1 to 31)

REFERENCE
AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H.,

n.P., Zimmerman, J. and Ecker, J.R.
 Genomic-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Published (2001)

act: Joseph R. Ecker
 Institute Genomic Analysis Laboratory (IGNAL)
 Salk Institute for Biological Studies
 10 N. Torrey Pines Road, La Jolla, CA 92037, USA
 858 453 4100 x1752
 858 558 6379

1: ecker@salk.edu
 is: single pass sequence recovered from the left border of
 this sequence lies within an annotated exon of At1g30970.
 is: TDNA tagged.

Location/Qualifiers

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/note="PCR was performed on Arabidopsis thaliana lines

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elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

47.9%; Score 13.4; DB 28; Length 31;

ilarity 73.9%; Pred. No. 2.9e+05; Indels 0; Gaps 0;
 Conservative 0; Mismatches 6;

ATCATCTCTGCATGTCAGGT 25

|||||

ATCATCACTGCATGCCAGTT 1

55117 42 bp DNA linear GSS 18-JUN-2002
 idopsis thaliana T-DNA flanking sequence GK-135B08-012755,
 mic survey sequence.

55117

55117.1 GI:21518160

idopsis thaliana (thale cress)

idopsis thaliana

aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

matophyta; Magnoliophyta; eudicotyledons; core eudicots;

ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

izhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Siedler, H.

Weishaar, B.

ipeline for automated high-throughput generation of FSTs

anking sequence tags) from Arabidopsis thaliana T-DNA

nsformed lines

ublished

so, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.

ew Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)

flanking sequence tag based reverse genetics

ublished

(bases 1 to 42)

Y., Rosso, M., Strizhov, N. and Weishaar, B.

ect Submission

mitted (17-JUN-2002) Weishaar B., Max-Planck-Institut fuer

chungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

s sequence is recovered from the left border of the T-DNA. It

icates an insertion within the locus defined by clone T209. The

ences are generated at the MPI for Plant Breeding Research in

context of the GABI-Kat project. GABI-Kat is part of the German

Plant Genomics program designated 'GABI'. Information or
 availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

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vector PAC161. The lines contain one or more T-DNA

insertions. The DNA fragment(s) resulting from

were directly sequenced to determine the genomic

flanking the insertion. Sequences displaying s

similarity to the A. thaliana nuclear genome s

processed for submission. T-DNA derived sequen

removed"

ORIGIN

Query Match 47.9%; Score 13.4; DB 29; Length 42;

Best Local Similarity 73.9%; Pred. No. 3.3e+05;

Matches 17; Conservative 0; Mismatches 6; Indels 0;

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|||||

Db 34 TTTCTCTCTCATGCCAGTCCA 12

RESULT 39

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LOCUS

DEFINITION

H92446 H92446.1 GI:1088024

Yt89b09.r1 Soares pineal gland N3HPG Homo sapiens cDNA

IMAGE:231449 5' similar to SP:A38409 A38409 NADH DEHYDR

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho

1 (bases 1 to 46)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Mar

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P.

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; con

IMAGE Consortium (info@image.lnl.gov) for further info

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert length: 859 Std Error: 0.00

Seq primer: M33RP1

High quality sequence stop: 1.

Location/Qualifiers

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FEATURES

source

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

cleic search, using sw model

April 12, 2004, 16:42:59 ; Search time 21.8462 Seconds
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US-10-090-326-23

28
1 agcatcatctcgtatggtcaggtcat 28

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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hits satisfying chosen parameters: 874574

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Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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is the number of results predicted by chance to have a
ratio than or equal to the score of the result being printed,
derived by analysis of the total score distribution.

SUMMARIES

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	55.7	30	2	US-08-819-458A-14	Sequence 14, Appl
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	52.9	50	3	US-09-315-886C-13	Sequence 13, Appl
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46.4	30	2	US-08-160-063-8	Sequence 8, Appl	217	12.8	45.7	60	4	US-09-559-671A-21	Sequence
46.4	30	3	US-08-473-313-8	Sequence 8, Appl	218	12.8	45.7	60	4	US-09-339-926A-21	Sequence
46.4	33	4	US-09-191-468-9	Sequence 9, Appl	219	12.8	45.7	60	4	US-07-703-421-12	Sequence
46.4	40	1	US-07-743-245-1	Sequence 187, App	220	12.6	45.0	20	1	US-08-008-006A-12	Sequence
46.4	54	4	US-09-479-645A-187	Sequence 4233, App	221	12.6	45.0	20	1	US-08-765-340-66	Sequence
46.4	54	4	US-09-747-259-39	Sequence 39, Appl	222	12.6	45.0	20	1	US-08-820-412-8	Sequence
46.4	58	4	US-09-422-978-4233	Sequence 4233, App	223	12.6	45.0	22	1	US-07-738-000-5	Sequence
45.7	18	4	US-09-226-568-5	Sequence 5, Appl	224	12.6	45.0	22	3	US-09-258-928-5	Sequence
45.7	20	3	US-07-967-693-42	Sequence 42, Appl	225	12.6	45.0	22	4	US-09-660-872A-5	Sequence
45.7	21	1	US-08-195-072-40	Sequence 40, Appl	226	12.6	45.0	22	4	US-09-592-595A-5	Sequence
45.7	21	1	US-08-195-735-40	Sequence 40, Appl	227	12.6	45.0	22	4	US-08-823-110-11	Sequence
45.7	21	1	US-08-195-747-40	Sequence 40, Appl	228	12.6	45.0	24	3	US-08-604-298-11	Sequence
45.7	21	1	US-08-446-884-40	Sequence 40, Appl	229	12.6	45.0	24	3	US-08-483-528B-68	Sequence
45.7	21	1	US-08-195-073-40	Sequence 40, Appl	230	12.6	45.0	25	2	US-08-483-528B-69	Sequence
45.7	21	1	US-08-198-175-40	Sequence 40, Appl	231	12.6	45.0	25	3	US-08-673-799C-68	Sequence
45.7	21	1	US-08-443-153-40	Sequence 40, Appl	232	12.6	45.0	25	3	US-08-673-799C-69	Sequence
45.7	21	2	US-08-442-807-40	Sequence 40, Appl	233	12.6	45.0	25	4	US-09-393-385B-69	Sequence
45.7	21	3	US-08-442-807-40	Sequence 40, Appl	234	12.6	45.0	25	4	US-09-393-385B-69	Sequence
45.7	23	3	US-08-986-331-2	Sequence 2, Appl	235	12.6	45.0	25	4	US-09-866-108A-3106	Sequence
45.7	25	1	US-08-495-743-47	Sequence 47, Appl	236	12.6	45.0	27	3	US-09-056-226-10	Sequence
45.7	25	1	US-08-495-739-47	Sequence 47, Appl	237	12.6	45.0	31	3	US-08-679-645-410	Sequence
45.7	25	3	US-08-495-741-47	Sequence 47, Appl	238	12.6	45.0	32	3	US-09-038-909-7	Sequence
45.7	25	3	US-08-062-023-47	Sequence 7, Appl	239	12.6	45.0	32	4	US-09-543-141-7	Sequence
45.7	26	4	US-09-787-628-7	Sequence 1221, App	240	12.6	45.0	33	4	US-09-417-197-91	Sequence
45.7	26	2	US-08-859-998-1221	Sequence 1221, App	241	12.6	45.0	36	1	US-08-368-803-21	Sequence
45.7	26	4	US-09-225-928-1221	Sequence 1221, App	242	12.6	45.0	36	2	US-08-578-096A-22	Sequence
45.7	27	3	US-09-225-201B-1221	Sequence 910, App	243	12.6	45.0	36	3	US-08-790-517-12	Sequence
45.7	27	3	US-08-985-162-910	Sequence 1054, App	244	12.6	45.0	36	3	US-09-240-426-22	Sequence
45.7	27	4	US-08-679-645-1054	Sequence 910, App	245	12.6	45.0	36	3	US-09-219-932-18	Sequence
45.7	27	4	US-09-401-063-910		246	12.6	45.0				

45.0	36	3	US-09-271-778-9	Sequence 9, Appli	C 320	12.4	44.3	32	3	US-08-870-930-4	Sequenc
45.0	36	4	US-09-362-831-22	Sequence 22, Appl	C 321	12.4	44.3	32	3	US-08-887-421-99	Sequenc
45.0	36	4	US-09-788-871-9	Sequence 9, Appli	C 322	12.4	44.3	32	3	US-08-973-124-44	Sequenc
45.0	37	3	US-08-726-807B-25	Sequence 25, Appl	C 323	12.4	44.3	32	3	US-08-973-124-187	Sequenc
45.0	37	3	US-09-258-367-25	Sequence 25, Appl	C 324	12.4	44.3	32	3	US-09-364-902-2	Sequenc
45.0	37	3	US-09-546-550-25	Sequence 25, Appl	C 325	12.4	44.3	32	3	US-09-275-850-40	Sequenc
45.0	37	3	US-09-431-414-25	Sequence 25, Appl	C 326	12.4	44.3	32	3	US-08-952-793-65	Sequenc
45.0	37	3	US-09-225-670-25	Sequence 25, Appl	C 327	12.4	44.3	32	4	US-09-363-939A-2	Sequenc
45.0	37	4	US-09-431-349C-25	Sequence 25, Appl	C 328	12.4	44.3	32	4	US-09-163-025B-3	Sequenc
45.0	37	4	US-09-450-072-49	Sequence 49, Appl	C 329	12.4	44.3	32	4	US-09-254-968-136	Sequenc
45.0	37	4	US-09-351-348-49	Sequence 49, Appl	C 330	12.4	44.3	32	4	US-09-849-928-65	Sequenc
45.0	39	1	US-08-481-003-14	Sequence 14, Appl	C 331	12.4	44.3	32	4	US-10-037-282-3	Sequenc
45.0	39	1	US-08-485-598-14	Sequence 14, Appl	C 332	12.4	44.3	32	4	US-09-854-662-2	Sequenc
45.0	40	4	US-08-952-445-33	Sequence 33, Appl	C 333	12.4	44.3	32	5	PCT-US95-12401A-3	Sequenc
45.0	41	4	US-09-468-872-20	Sequence 20, Appl	C 334	12.4	44.3	32	5	PCT-US96-08014-44	Sequenc
45.0	43	4	US-09-136-421-1	Sequence 1, Appli	C 335	12.4	44.3	32	5	PCT-US96-08014-187	Sequenc
45.0	45	3	US-08-997-918-15	Sequence 15, Appl	C 336	12.4	44.3	32	5	PCT-US96-09455A-65	Sequenc
45.0	45	4	US-08-979-608A-30	Sequence 30, Appl	C 337	12.4	44.3	32	5	PCT-US96-09472-77	Sequenc
45.0	45	4	US-09-517-849-30	Sequence 30, Appl	C 338	12.4	44.3	32	5	PCT-US96-09537-2	Sequenc
45.0	45	4	US-09-616-289-30	Sequence 30, Appl	C 339	12.4	44.3	33	2	US-08-488-402A-2	Sequenc
45.0	46	4	US-09-522-732B-21	Sequence 21, Appl	C 340	12.4	44.3	33	2	US-08-484-552A-2	Sequenc
45.0	47	2	US-08-600-783-15	Sequence 15, Appl	C 341	12.4	44.3	33	5	PCT-US96-09472-2	Sequenc
45.0	47	4	US-09-422-978-83	Sequence 83, Appl	C 342	12.4	44.3	34	4	US-09-522-217-57	Sequenc
45.0	50	4	US-09-443-199C-905	Sequence 906, App	C 343	12.4	44.3	34	4	US-09-923-246-57	Sequenc
45.0	51	1	US-08-248-016-3	Sequence 3, Appli	C 344	12.4	44.3	34	4	US-10-295-723-57	Sequenc
45.0	51	1	US-08-451-501-3	Sequence 3, Appli	C 345	12.4	44.3	35	1	US-08-283-067-5	Sequenc
45.0	51	1	US-08-379-926A-2	Sequence 2, Appli	C 346	12.4	44.3	35	1	US-08-283-067-25	Sequenc
45.0	51	1	US-08-379-926A-3	Sequence 3, Appli	C 347	12.4	44.3	35	1	US-08-447-411-77	Sequenc
45.0	51	2	US-08-642-541-7	Sequence 7, Appli	C 348	12.4	44.3	35	3	US-09-232-479-2	Sequenc
45.0	51	3	US-09-260-889-7	Sequence 7, Appli	C 349	12.4	44.3	35	4	US-09-784-990-2	Sequenc
45.0	51	4	US-09-479-275-4	Sequence 4, Appli	C 350	12.4	44.3	38	2	US-08-640-732-12	Sequenc
45.0	51	5	PCT-US95-06761-3	Sequence 3, Appli	C 351	12.4	44.3	38	5	PCT-US94-12778-12	Sequenc
45.0	52	2	US-08-713-455A-2	Sequence 2, Appli	C 352	12.4	44.3	39	1	US-08-481-003-1	Sequenc
45.0	54	1	US-08-060-822A-16	Sequence 16, Appl	C 353	12.4	44.3	39	3	US-08-485-598-1	Sequenc
45.0	54	1	US-08-060-822A-17	Sequence 17, Appl	C 354	12.4	44.3	40	1	US-08-317-403A-5	Sequenc
45.0	54	5	PCT-US94-05257-16	Sequence 16, Appl	C 355	12.4	44.3	40	1	US-08-471-985A-5	Sequenc
45.0	54	5	PCT-US94-05257-17	Sequence 17, Appl	C 356	12.4	44.3	40	1	US-08-433-126A-4	Sequenc
44.3	22	3	US-08-882-046-18	Sequence 18, Appl	C 357	12.4	44.3	40	1	US-08-433-124A-4	Sequenc
44.3	22	3	US-08-882-046-83	Sequence 8, Appli	C 358	12.4	44.3	40	2	US-08-477-527A-4	Sequenc
44.3	29	1	US-08-538-875-3	Sequence 3, Appli	C 359	12.4	44.3	40	3	US-08-481-710-4	Sequenc
44.3	29	4	US-09-304-232-371	Sequence 371, App	C 360	12.4	44.3	40	3	US-08-976-413A-4	Sequenc
44.3	30	1	US-08-484-557C-55	Sequence 55, Appl	C 361	12.4	44.3	40	5	PCT-US95-12401A-5	Sequenc
44.3	30	1	US-08-487-426B-55	Sequence 55, Appl	C 362	12.4	44.3	40	5	PCT-US96-06059-4	Sequenc
44.3	30	2	US-08-487-720A-55	Sequence 55, Appl	C 363	12.4	44.3	40	5	PCT-US96-09537-4	Sequenc
44.3	30	3	US-09-258-797-74	Sequence 74, Appl	C 364	12.4	44.3	41	1	US-08-368-803-15	Sequenc
44.3	31	1	US-08-095-726-66	Sequence 66, Appl	C 365	12.4	44.3	41	2	US-08-578-096A-17	Sequenc
44.3	31	1	US-08-096-043-63	Sequence 63, Appl	C 366	12.4	44.3	41	3	US-08-790-517-18	Sequenc
44.3	31	1	US-08-096-623A-71	Sequence 71, Appl	C 367	12.4	44.3	41	3	US-09-240-426-17	Sequenc
44.3	31	2	US-08-205-304-4	Sequence 4, Appli	C 368	12.4	44.3	41	3	US-09-219-932-24	Sequenc
44.3	31	2	US-08-859-598-238	Sequence 238, App	C 369	12.4	44.3	41	4	US-09-362-831-28	Sequenc
44.3	31	4	US-09-225-928-238	Sequence 238, App	C 370	12.4	44.3	42	3	US-08-938-830-30	Sequenc
44.3	31	4	US-09-225-201B-238	Sequence 238, App	C 371	12.4	44.3	43	1	US-08-475-063-35	Sequenc
44.3	32	1	US-08-399-412A-5	Sequence 5, Appli	C 372	12.4	44.3	43	1	US-08-207-792-35	Sequenc
44.3	32	1	US-08-317-403A-3	Sequence 3, Appli	C 373	12.4	44.3	43	3	US-08-732-708C-9	Sequenc
44.3	32	1	US-08-384-708A-99	Sequence 99, Appl	C 374	12.4	44.3	43	4	US-09-232-946-1	Sequenc
44.3	32	1	US-08-471-985A-3	Sequence 3, Appli	C 375	12.4	44.3	46	1	US-08-095-726-42	Sequenc
44.3	32	1	US-08-488-423A-44	Sequence 44, Appl	C 376	12.4	44.3	46	1	US-08-096-043-39	Sequenc
44.3	32	1	US-08-458-424B-44	Sequence 44, Appl	C 377	12.4	44.3	46	1	US-08-093-577-35	Sequenc
44.3	32	1	US-08-472-255A-65	Sequence 65, Appl	C 378	12.4	44.3	46	1	US-08-096-623A-47	Sequenc
44.3	32	1	US-08-479-724A-65	Sequence 65, Appl	C 379	12.4	44.3	47	4	US-09-422-978-1386	Sequenc
44.3	32	1	US-08-447-169A-61	Sequence 61, Appl	C 380	12.4	44.3	47	4	US-09-422-978-1941	Sequenc
44.3	32	2	US-08-488-402A-77	Sequence 77, Appl	C 381	12.4	44.3	50	2	US-08-850-049-122	Sequenc
44.3	32	2	US-08-465-591A-2	Sequence 2, Appli	C 382	12.4	44.3	50	2	US-08-050-478-122	Sequenc
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44.3	32	2	US-08-233-012C-61	Sequence 61, Appl	C 384	12.4	44.3	50	3	US-09-414-117-122	Sequenc
44.3	32	2	US-08-484-552A-77	Sequence 77, Appl	C 385	12.4	44.3	50	4	US-09-678-437-122	Sequenc
44.3	32	2	US-08-792-075-2	Sequence 2, Appli	C 386	12.4	44.3	50	4	US-09-613-263-13	Sequenc
44.3	32	2	US-08-477-527A-2	Sequence 2, Appli	C 387	12.4	44.3	51	4	US-09-068-740A-34	Sequenc
44.3	32	2	US-08-894-578-105	Sequence 105, App	C 388	12.4	44.3	51	4	US-09-640-198D-6	Sequenc
44.3	32	3	US-08-472-256B-65	Sequence 65, Appl	C 389	12.4	44.3	52	2	US-09-639-667-23	Sequenc
44.3	32	3	US-08-481-710-2	Sequence 2, Appli	C 390	12.4	44.3	52	2	US-08-829-876-68	Sequenc
44.3	32	3	US-09-046-247-4	Sequence 4, Appli	C 391	12.4	44.3	52	4	US-09-234-874A-68	Sequenc
44.3	32	3	US-09-023-228B-3	Sequence 3, Appli	C 392	12.4	44.3	52	4	US-09-234-873A-68	Sequenc

44.3	54	2	US-08-452-724A-15	Sequence 15, Appl	466	12.2	43.6	35	4	US-09-530-139-66	Sequenc
44.3	54	4	US-08-453-623-15	Sequence 15, Appl	c 467	12.2	43.6	35	5	PCT-US93-01009-21	Sequenc
44.3	56	3	US-09-091-814-49	Sequence 49, Appl	468	12.2	43.6	36	3	US-08-941-445A-2	Sequenc
44.3	58	4	US-09-214-278-28	Sequence 28, Appl	c 469	12.2	43.6	39	1	US-08-120-607A-5	Sequenc
44.3	58	4	US-09-895-722-28	Sequence 28, Appl	c 470	12.2	43.6	39	2	US-08-453-848-5	Sequenc
44.3	58	4	US-09-723-368-26	Sequence 26, Appl	c 471	12.2	43.6	39	3	US-09-169-027-5	Sequenc
44.3	60	1	US-08-036-555B-167	Sequence 167, App	c 472	12.2	43.6	39	4	US-09-545-481-6	Sequenc
44.3	60	1	US-08-469-569-167	Sequence 167, App	c 473	12.2	43.6	40	2	US-08-713-815A-6	Sequenc
44.3	60	1	US-08-249-322A-167	Sequence 167, App	c 474	12.2	43.6	40	4	US-09-918-696-45	Sequenc
44.3	60	1	US-08-469-526A-167	Sequence 167, App	c 475	12.2	43.6	40	4	US-09-918-696-46	Sequenc
44.3	60	2	US-08-734-591A-167	Sequence 167, App	476	12.2	43.6	40	5	PCT-US94-08052-9	Sequenc
44.3	60	2	US-08-469-660-167	Sequence 167, App	477	12.2	43.6	41	4	US-08-813-507-114	Sequenc
44.3	60	3	US-08-470-335-167	Sequence 167, App	478	12.2	43.6	41	4	US-09-464-453-114	Sequenc
44.3	60	3	US-08-735-021-167	Sequence 167, App	c 479	12.2	43.6	45	1	US-07-884-811-21	Sequenc
44.3	60	3	US-08-734-664A-167	Sequence 167, App	c 480	12.2	43.6	45	1	US-07-885-971-21	Sequenc
44.3	60	3	US-08-470-339-167	Sequence 167, App	c 481	12.2	43.6	45	1	US-08-087-783A-21	Sequenc
44.3	60	4	US-08-467-602-167	Sequence 167, App	c 482	12.2	43.6	45	1	US-08-194-088B-21	Sequenc
44.3	60	5	PCT-US94-05083C-163	Sequence 163, App	c 483	12.2	43.6	45	1	US-08-435-501-20	Sequenc
44.3	60	5	PCT-US95-06846A-167	Sequence 167, App	c 484	12.2	43.6	45	1	US-08-435-764-20	Sequenc
43.6	18	4	US-08-621-700-10	Sequence 10, Appl	c 485	12.2	43.6	45	1	US-08-792-078-20	Sequenc
43.6	18	4	US-08-929-940-10	Sequence 10, Appl	c 486	12.2	43.6	45	1	US-08-482-882-46	Sequenc
43.6	18	4	US-09-625-972-13	Sequence 13, Appl	c 487	12.2	43.6	45	1	US-08-483-389-46	Sequenc
43.6	18	5	PCT-US95-03940-10	Sequence 10, Appl	c 488	12.2	43.6	45	2	US-08-487-113D-46	Sequenc
43.6	19	4	US-09-672-717-147	Sequence 147, App	c 489	12.2	43.6	45	2	US-08-473-503-46	Sequenc
43.6	20	1	US-08-735-963-9	Sequence 9, Appli	c 490	12.2	43.6	45	2	US-08-194-087-21	Sequenc
43.6	20	2	US-09-105-057-9	Sequence 9, Appli	c 491	12.2	43.6	45	2	US-08-483-932-46	Sequenc
43.6	20	3	US-09-304-214-9	Sequence 9, Appli	c 492	12.2	43.6	45	2	US-08-720-420A-46	Sequenc
43.6	20	4	US-09-423-890-17	Sequence 17, Appl	c 493	12.2	43.6	45	3	US-08-714-017-46	Sequenc
43.6	20	4	US-09-198-452A-5100	Sequence 5100, Ap	c 494	12.2	43.6	45	3	US-08-475-680-46	Sequenc
43.6	21	4	US-08-757-223-3	Sequence 3, Appli	c 495	12.2	43.6	45	5	PCT-US93-04648-21	Sequenc
43.6	22	3	US-08-480-173A-3	Sequence 3, Appli	c 496	12.2	43.6	45	5	PCT-US93-04717-20	Sequenc
43.6	22	3	US-08-484-408A-3	Sequence 3, Appli	c 497	12.2	43.6	46	1	US-08-441-430-29	Sequenc
43.6	22	4	US-09-468-872-48	Sequence 48, Appl	c 498	12.2	43.6	46	3	US-09-357-541-5	Sequenc
43.6	23	3	US-09-357-541-7	Sequence 7, Appli	c 499	12.2	43.6	46	3	US-09-357-541-6	Sequenc
43.6	23	3	US-09-357-541-8	Sequence 8, Appli	c 500	12.2	43.6	47	4	US-09-422-978-891	Sequenc
43.6	25	4	US-09-398-858-29	Sequence 29, Appl	c 501	12.2	43.6	47	4	US-09-422-978-1869	Sequenc
43.6	25	4	US-09-866-108A-12932	Sequence 12932, A	c 502	12.2	43.6	47	4	US-09-422-978-3197	Sequenc
43.6	25	4	US-09-866-108A-12933	Sequence 12933, A	c 503	12.2	43.6	49	4	US-09-400-541-10	Sequenc
43.6	27	1	US-08-232-538-4	Sequence 4, Appli	c 504	12.2	43.6	49	4	US-09-899-999-10	Sequenc
43.6	27	2	US-08-786-164-4	Sequence 4, Appli	c 505	12.2	43.6	50	2	US-08-615-961-7	Sequenc
43.6	27	3	US-08-985-162-1169	Sequence 1169, Ap	c 506	12.2	43.6	50	4	US-09-627-562A-1	Sequenc
43.6	27	3	US-08-584-040-3177	Sequence 3177, Ap	c 507	12.2	43.6	50	4	US-08-912-378A-1	Sequenc
43.6	27	4	US-08-584-040-3456	Sequence 3456, Ap	c 508	12.2	43.6	51	4	US-08-218-369-5	Sequenc
43.6	27	4	US-08-584-040-4627	Sequence 4627, Ap	c 509	12.2	43.6	51	4	US-08-218-369-14	Sequenc
43.6	27	4	US-08-584-040-4725	Sequence 4725, Ap	c 510	12.2	43.6	51	4	US-09-443-199C-166	Sequenc
43.6	27	4	US-09-398-858-27	Sequence 27, Appl	c 511	12.2	43.6	51	4	US-09-443-199C-1148	Sequenc
43.6	27	4	US-09-401-063-1169	Sequence 1169, Ap	c 512	12.2	43.6	51	4	US-09-904-599A-5	Sequenc
43.6	28	4	US-09-598-218-1	Sequence 1, Appli	c 513	12.2	43.6	51	5	PCT-US95-03742-5	Sequenc
43.6	29	1	US-08-293-086-8	Sequence 8, Appli	c 514	12.2	43.6	51	5	PCT-US95-03742-14	Sequenc
43.6	29	1	US-08-244-938-8	Sequence 8, Appli	c 515	12.2	43.6	51	5	PCT-US96-03916-25	Sequenc
43.6	29	2	US-08-861-306-8	Sequence 8, Appli	c 516	12.2	43.6	52	3	US-09-081-702-14	Sequenc
43.6	29	2	US-08-468-037A-35	Sequence 35, Appl	c 517	12.2	43.6	52	4	US-08-956-171B-1925	Sequenc
43.6	29	2	US-08-471-973A-35	Sequence 35, Appl	c 518	12.2	43.6	54	1	US-08-386-579-12	Sequenc
43.6	29	2	US-08-465-880-16	Sequence 16, Appl	c 519	12.2	43.6	54	1	US-08-665-055-6	Sequenc
43.6	29	3	US-09-035-357-35	Sequence 35, Appl	c 520	12.2	43.6	54	3	US-08-342-924-11	Sequenc
43.6	29	3	US-09-016-520-17	Sequence 17, Appl	c 521	12.2	43.6	54	3	US-08-342-924-18	Sequenc
43.6	29	3	US-09-144-611-8	Sequence 8, Appli	c 522	12.2	43.6	54	3	US-08-960-111-17	Sequenc
43.6	29	3	US-09-130-973-17	Sequence 17, Appl	c 523	12.2	43.6	54	3	US-08-960-111-20	Sequenc
43.6	29	3	US-09-477-902-17	Sequence 17, Appl	c 524	12.2	43.6	54	3	US-09-326-840-6	Sequenc
43.6	29	4	US-09-453-514A-8	Sequence 8, Appli	c 525	12.2	43.6	54	3	US-08-665-057-6	Sequenc
43.6	29	4	US-09-135-202-35	Sequence 35, Appl	c 526	12.2	43.6	54	3	US-09-490-774-17	Sequenc
43.6	29	4	US-08-802-331-16	Sequence 16, Appl	c 527	12.2	43.6	54	3	US-09-490-774-20	Sequenc
43.6	29	4	US-09-389-283-35	Sequence 35, Appl	c 528	12.2	43.6	54	4	US-08-299-931-3	Sequenc
43.6	29	4	US-09-370-541-11	Sequence 11, Appl	c 529	12.2	43.6	54	4	US-09-191-468-17	Sequenc
43.6	32	4	US-09-354-231B-25	Sequence 25, Appl	c 530	12.2	43.6	54	4	US-09-892-058A-6	Sequenc
43.6	32	4	US-09-128-602B-25	Sequence 25, Appl	c 531	12.2	43.6	54	5	PCT-US96-01807-12	Sequenc
43.6	32	4	US-09-995-297-25	Sequence 25, Appl	c 532	12.2	43.6	58	3	US-09-248-643-13	Sequenc
43.6	33	1	US-08-463-224-61	Sequence 61, Appl	c 533	12.2	43.6	58	4	US-09-591-025-7	Sequenc
43.6	33	2	US-08-463-377-61	Sequence 61, Appl	c 534	12.2	43.6	58	4	US-09-894-927B-7	Sequenc
43.6	34	3	US-09-232-478-18	Sequence 18, Appl	c 535	12.2	43.6	59	1	US-08-482-882-91	Sequenc
43.6	34	4	US-09-785-055-18	Sequence 18, Appl	c 536	12.2	43.6	59	1	US-08-270-805C-18	Sequenc
43.6	35	3	US-08-483-511-21	Sequence 21, Appl	c 537	12.2	43.6	59	1	US-08-483-389-91	Sequenc
43.6	35	4	US-09-823-823-41	Sequence 41, Appl	c 538	12.2	43.6	59	2	US-08-410-654B-18	Sequenc

43.6	59	2	US-08-474-851-18	Sequence 18, Appl	c 612	12	42.9	37	1	US-08-428-733A-7	Sequence
43.6	59	2	US-08-481-560-18	Sequence 18, Appl	c 613	12	42.9	37	1	US-08-428-733A-38	Sequence
43.6	59	2	US-08-487-113D-91	Sequence 91, Appl	c 614	12	42.9	37	1	US-08-428-733A-39	Sequence
43.6	59	2	US-08-473-503-91	Sequence 91, Appl	c 615	12	42.9	38	1	US-08-464-339A-5	Sequence
43.6	59	2	US-08-483-932-91	Sequence 91, Appl	c 616	12	42.9	38	2	US-08-899-324-19	Sequence
43.6	59	2	US-08-720-420A-91	Sequence 91, Appl	c 617	12	42.9	38	3	US-08-329-892B-19	Sequence
43.6	59	2	US-08-714-017-91	Sequence 91, Appl	c 618	12	42.9	39	6	5223482-34	Patent No.
43.6	59	3	US-08-475-680-91	Sequence 91, Appl	c 619	12	42.9	40	3	US-09-262-773-148	Sequence
43.6	59	3	US-08-643-810A-18	Sequence 18, Appl	c 620	12	42.9	40	3	US-09-306-998-28	Sequence
43.6	60	3	US-09-023-228B-117	Sequence 117, Appl	c 621	12	42.9	40	4	US-09-317-789-3	Sequence
43.6	60	4	US-09-163-025B-117	Sequence 117, Appl	c 622	12	42.9	42	1	US-08-168-917-23	Sequence
43.6	60	4	US-10-037-282-117	Sequence 117, Appl	c 623	12	42.9	42	2	US-08-460-510-23	Sequence
43.6	60	6	5194425-8	Patent No. 5194425	c 624	12	42.9	42	2	US-08-460-490-23	Sequence
42.9	20	3	US-08-765-340-67	Sequence 67, Appl	c 625	12	42.9	42	5	PCT-US92-00730-23	Sequence
42.9	20	4	US-09-705-267A-168	Sequence 168, App	c 626	12	42.9	42	5	PCT-US92-10430-18	Sequence
42.9	20	4	US-09-843-376-36	Sequence 36, Appl	c 627	12	42.9	43	3	US-08-732-708C-6	Sequence
42.9	21	2	US-08-117-952-402	Sequence 402, App	c 628	12	42.9	43	3	US-08-732-708C-16	Sequence
42.9	21	2	US-08-863-639A-45	Sequence 45, Appl	c 629	12	42.9	43	3	US-08-732-708C-17	Sequence
42.9	21	2	US-08-863-639A-49	Sequence 49, Appl	c 630	12	42.9	43	4	US-09-313-221A-8	Sequence
42.9	21	2	US-08-863-639A-82	Sequence 82, Appl	c 631	12	42.9	45	1	US-08-168-917-20	Sequence
42.9	21	2	US-08-863-639A-86	Sequence 86, Appl	c 632	12	42.9	45	1	US-08-168-917-22	Sequence
42.9	21	4	US-09-676-610B-8	Sequence 8, Appl	c 633	12	42.9	45	2	US-08-460-510-20	Sequence
42.9	21	4	US-09-422-978-10737	Sequence 10737, A	c 634	12	42.9	45	2	US-08-460-510-22	Sequence
42.9	23	2	US-08-355-138-22	Sequence 22, Appl	c 635	12	42.9	45	2	US-08-460-490-20	Sequence
42.9	23	4	US-09-504-132-16	Sequence 16, Appl	c 636	12	42.9	45	2	US-08-460-490-22	Sequence
42.9	24	2	US-08-763-762-2	Sequence 2, Appl	c 637	12	42.9	45	4	US-09-383-143-23	Sequence
42.9	24	2	US-08-859-998-877	Sequence 877, App	c 638	12	42.9	45	4	US-09-383-143-24	Sequence
42.9	24	3	US-09-123-012-2	Sequence 2, Appl	c 639	12	42.9	45	4	US-09-518-914-11	Sequence
42.9	24	4	US-09-225-928-877	Sequence 877, App	c 640	12	42.9	45	5	PCT-US92-00730-20	Sequence
42.9	24	4	US-09-608-701B-6	Sequence 6, Appl	c 641	12	42.9	45	5	PCT-US92-00730-22	Sequence
42.9	24	4	US-09-225-2018-877	Sequence 877, App	c 642	12	42.9	45	5	PCT-US92-10430-15	Sequence
42.9	25	3	US-08-513-974B-201	Sequence 201, App	c 643	12	42.9	45	5	PCT-US92-10430-17	Sequence
42.9	25	4	US-09-866-108A-14950	Sequence 14950, A	c 644	12	42.9	46	2	US-08-596-387B-63	Sequence
42.9	25	4	US-09-866-108A-14951	Sequence 14951, A	c 645	12	42.9	46	2	US-08-596-387B-64	Sequence
42.9	25	4	US-09-866-108A-14952	Sequence 14952, A	c 646	12	42.9	46	4	US-09-067-615-63	Sequence
42.9	25	4	US-09-866-108A-14953	Sequence 14953, A	c 647	12	42.9	46	4	US-09-067-615-64	Sequence
42.9	25	4	US-09-866-108A-14954	Sequence 14954, A	c 648	12	42.9	46	5	PCT-US95-09816A-63	Sequence
42.9	25	4	US-09-866-108A-14955	Sequence 14955, A	c 649	12	42.9	46	5	PCT-US95-09816A-64	Sequence
42.9	27	3	US-08-325-426B-10	Sequence 10, Appl	c 650	12	42.9	47	4	US-09-486-241-7	Sequence
42.9	27	3	US-08-985-162-1301	Sequence 1301, Ap	c 651	12	42.9	47	4	US-09-422-978-1615	Sequence
42.9	27	4	US-08-584-040-3457	Sequence 3457, Ap	c 652	12	42.9	47	4	US-09-422-978-3595	Sequence
42.9	27	4	US-08-584-040-5230	Sequence 5230, Ap	c 653	12	42.9	48	1	US-08-168-917-21	Sequence
42.9	27	4	US-09-401-063-1301	Sequence 1301, Ap	c 654	12	42.9	48	2	US-08-460-510-21	Sequence
42.9	29	4	US-08-845-381B-9	Sequence 9, Appl	c 655	12	42.9	48	2	US-08-460-490-21	Sequence
42.9	30	2	US-08-850-049-88	Sequence 88, Appl	c 656	12	42.9	48	5	PCT-US92-00730-21	Sequence
42.9	30	3	US-08-050-478-88	Sequence 88, Appl	c 657	12	42.9	48	5	PCT-US92-10430-16	Sequence
42.9	30	3	US-08-821-451A-21	Sequence 21, Appl	c 658	12	42.9	50	4	US-09-554-929-64	Sequence
42.9	30	3	US-09-263-810-21	Sequence 21, Appl	c 659	12	42.9	50	4	US-08-956-171E-2135	Sequence
42.9	30	3	US-07-901-713A-5	Sequence 5, Appl	c 660	12	42.9	51	2	US-09-061-337-13	Sequence
42.9	30	3	US-09-414-117-88	Sequence 88, Appl	c 661	12	42.9	51	2	US-09-122-123-13	Sequence
42.9	30	4	US-09-743-211-13	Sequence 13, Appl	c 662	12	42.9	51	3	US-09-340-991-13	Sequence
42.9	30	4	US-09-583-169-21	Sequence 21, Appl	c 663	12	42.9	51	3	US-08-974-609-13	Sequence
42.9	31	3	US-09-678-437-88	Sequence 88, Appl	c 664	12	42.9	51	4	US-09-549-098-13	Sequence
42.9	31	3	US-08-586-039B-42	Sequence 42, Appl	c 665	12	42.9	53	4	US-09-136-080B-50	Sequence
42.9	31	4	US-09-699-769-42	Sequence 42, Appl	c 666	12	42.9	53	4	US-09-549-098-13	Sequence
42.9	32	1	US-08-628-665-13	Sequence 13, Appl	c 667	12	42.9	54	1	US-08-311-486C-1038	Sequence
42.9	32	1	US-08-845-381B-11	Sequence 11, Appl	c 668	12	42.9	54	4	US-09-479-645A-191	Sequence
42.9	33	3	US-09-258-797-67	Sequence 67, Appl	c 669	12	42.9	59	4	US-09-532-656-10	Sequence
42.9	33	3	US-09-113-750A-54	Sequence 54, Appl	c 670	12	42.9	60	3	US-08-643-704A-2	Sequence
42.9	33	5	PCT-US96-09451-67	Sequence 67, Appl	c 671	12	42.9	60	3	US-08-643-704A-23	Sequence
42.9	34	1	US-08-628-665-15	Sequence 15, Appl	c 672	12	42.9	60	4	US-09-339-913B-41	Sequence
42.9	34	2	US-08-988-128-10	Sequence 10, Appl	c 673	12	42.9	60	4	US-09-339-904A-41	Sequence
42.9	35	4	US-08-483-941-8	Sequence 8, Appl	c 674	12	42.9	60	4	US-08-769-062B-41	Sequence
42.9	36	1	US-08-411-796-250	Sequence 250, App	c 675	12	42.9	60	4	US-09-344-002B-41	Sequence
42.9	36	3	US-08-471-039-250	Sequence 250, App	c 676	12	42.9	60	4	US-09-559-565C-41	Sequence
42.9	36	3	US-09-382-616A-26	Sequence 26, Appl	c 677	12	42.9	60	4	US-09-693-389-41	Sequence
42.9	36	3	US-09-382-616A-28	Sequence 28, Appl	c 678	12	42.9	60	4	US-08-845-381E-60	Sequence
42.9	36	4	US-08-655-15	Sequence 15, Appl	c 679	12	42.9	60	4	US-09-559-671A-41	Sequence
42.9	36	4	US-08-559-390-250	Sequence 250, App	c 680	12	42.9	60	4	US-09-852-385-6	Sequence
42.9	36	4	US-09-728-466-26	Sequence 26, Appl	c 681	12	42.9	60	4	US-09-339-928A-41	Sequence
42.9	36	5	PCT-US93-11198-250	Sequence 250, App	c 682	11.8	42.1	15	4	US-09-479-122-30	Sequence
42.9	37	1	US-08-474-542A-234	Sequence 234, App	c 683	11.8	42.1	15	4	US-09-481-997-30	Sequence
42.9	37	1	US-08-457-648-234	Sequence 234, App	c 684	11.8	42.1	15	4	US-09-484-355-30	Sequence

42.1	15	4	US-09-481-282-30	Sequence 30, Appl	c 758	11.8	42.1	30	5	PCT-US94-06066-20	Sequenc
42.1	15	4	US-09-455-659A-30	Sequence 30, Appl	c 759	11.8	42.1	31	4	US-09-402-214-51	Sequenc
42.1	15	4	US-09-484-996-30	Sequence 30, Appl	c 760	11.8	42.1	32	1	US-08-244-469-3	Sequenc
42.1	15	4	US-09-479-123-30	Sequence 30, Appl	c 761	11.8	42.1	33	1	US-08-102-567-2	Sequenc
42.1	17	1	US-08-281-940-26	Sequence 26, Appl	c 762	11.8	42.1	33	2	US-08-410-654B-38	Sequenc
42.1	17	1	US-08-281-940-65	Sequence 65, Appl	c 763	11.8	42.1	33	2	US-08-474-851-38	Sequenc
42.1	17	2	US-08-710-134-26	Sequence 26, Appl	c 764	11.8	42.1	33	2	US-08-481-560-38	Sequenc
42.1	17	2	US-08-710-134-65	Sequence 65, Appl	c 765	11.8	42.1	33	3	US-08-462-947-2	Sequenc
42.1	17	2	US-08-485-885-26	Sequence 26, Appl	c 766	11.8	42.1	33	3	US-08-713-404A-4	Sequenc
42.1	17	2	US-08-485-885-65	Sequence 65, Appl	c 767	11.8	42.1	33	4	US-09-475-460A-29	Sequenc
42.1	17	3	US-09-295-186-15	Sequence 15, Appl	c 768	11.8	42.1	33	4	US-09-748-061A-29	Sequenc
42.1	18	1	US-08-241-465B-16	Sequence 16, Appl	c 769	11.8	42.1	34	1	US-09-387-418A-4	Sequenc
42.1	18	3	US-09-339-993-26	Sequence 26, Appl	c 770	11.8	42.1	35	1	US-08-464-523B-17	Sequenc
42.1	18	4	US-09-303-069-22	Sequence 22, Appl	c 771	11.8	42.1	36	4	US-09-463-282B-25	Sequenc
42.1	19	1	US-08-077-619-6	Sequence 6, Appl	c 772	11.8	42.1	37	3	US-08-445-463B-35	Sequenc
42.1	19	1	US-08-127-954-30	Sequence 30, Appl	c 773	11.8	42.1	37	3	US-08-445-463C-35	Sequenc
42.1	19	2	US-08-379-078-708	Sequence 708, Appl	c 774	11.8	42.1	37	4	US-08-044-857D-35	Sequenc
42.1	19	2	US-08-538-711A-18	Sequence 18, Appl	c 775	11.8	42.1	37	5	PCT-US94-01437-35	Sequenc
42.1	19	3	US-08-725-027-18	Sequence 18, Appl	c 776	11.8	42.1	38	2	US-08-419-075-23	Sequenc
42.1	19	4	US-07-974-409C-292	Sequence 22, App	c 777	11.8	42.1	39	4	US-09-586-536-3	Sequenc
42.1	19	4	US-09-052-753B-10	Sequence 10, Appl	c 778	11.8	42.1	39	4	US-09-657-931A-14	Sequenc
42.1	19	4	US-09-542-552-18	Sequence 18, Appl	c 779	11.8	42.1	40	3	US-09-262-773-109	Sequenc
42.1	19	5	PCT-US93-00977-292	Sequence 292, App	c 780	11.8	42.1	40	3	US-09-060-299-277	Sequenc
42.1	20	3	US-09-490-692-110	Sequence 110, App	c 781	11.8	42.1	40	4	US-09-402-923A-277	Sequenc
42.1	20	4	US-09-780-175-83	Sequence 83, Appl	c 782	11.8	42.1	41	1	US-08-525-654B-139	Sequenc
42.1	20	4	US-09-658-688A-58	Sequence 58, Appl	c 783	11.8	42.1	41	1	US-08-481-003-6	Sequenc
42.1	20	4	US-08-422-978-11766	Sequence 11766, A	c 784	11.8	42.1	41	3	US-08-485-598-6	Sequenc
42.1	20	4	US-09-060-299-276	Sequence 276, App	c 785	11.8	42.1	42	1	US-08-281-940-62	Sequenc
42.1	20	4	US-09-402-923A-276	Sequence 276, App	c 786	11.8	42.1	43	4	US-09-425-638A-127	Sequenc
42.1	20	4	US-10-027-983-56	Sequence 56, Appl	c 787	11.8	42.1	43	4	US-09-543-004-127	Sequenc
42.1	20	6	5194428-8	Patent No. 5194428	c 788	11.8	42.1	47	1	US-08-458-084-13	Sequenc
42.1	20	6	5194428-9	Patent No. 5194428	c 789	11.8	42.1	47	1	US-08-305-508-13	Sequenc
42.1	21	4	US-09-780-175-4	Sequence 4, Appl	c 790	11.8	42.1	47	2	US-08-790-963-54	Sequenc
42.1	22	1	US-08-271-946A-26	Sequence 26, Appl	c 791	11.8	42.1	47	2	US-08-790-963-56	Sequenc
42.1	22	1	US-08-271-946A-60	Sequence 60, Appl	c 792	11.8	42.1	47	2	US-09-371-774-54	Sequenc
42.1	22	3	US-08-779-916A-26	Sequence 26, Appl	c 793	11.8	42.1	47	3	US-09-371-774-56	Sequenc
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42.1	22	3	US-08-750-232-26	Sequence 26, Appl	c 795	11.8	42.1	47	4	US-09-422-978-1774	Sequenc
42.1	22	3	US-08-750-232-60	Sequence 60, Appl	c 796	11.8	42.1	47	5	PCT-US95-02945-13	Sequenc
42.1	22	3	US-09-479-005A-1178	Sequence 1178, Ap	c 797	11.8	42.1	48	4	US-09-624-693A-25	Sequenc
42.1	22	5	PCT-US95-08604-26	Sequence 26, Appl	c 798	11.8	42.1	48	4	US-08-704-867A-6	Sequenc
42.1	22	5	PCT-US95-08606-26	Sequence 26, Appl	c 799	11.8	42.1	49	2	US-08-726-528A-7	Sequenc
42.1	22	5	PCT-US95-08606-60	Sequence 60, Appl	c 800	11.8	42.1	49	3	US-08-434-099A-12	Sequenc
42.1	23	3	US-08-749-527-3	Sequence 3, Appl	c 801	11.8	42.1	49	4	US-08-897-956A-30	Sequenc
42.1	24	4	US-09-463-702A-16	Sequence 16, Appl	c 802	11.8	42.1	51	4	US-09-443-199C-717	Sequenc
42.1	24	4	US-09-693-135-16	Sequence 16, Appl	c 803	11.8	42.1	53	3	US-08-818-112-146	Sequenc
42.1	25	4	US-09-866-108A-12930	Sequence 12930, A	c 805	11.8	42.1	53	4	US-09-056-556-146	Sequenc
42.1	25	4	US-08-643-704A-32	Sequence 32, Appl	c 806	11.8	42.1	53	4	US-09-056-556-205	Sequenc
42.1	26	3	US-08-914-421-6	Sequence 6, Appl	c 807	11.8	42.1	53	4	US-09-072-596-141	Sequenc
42.1	26	3	US-08-683-403-6	Sequence 6, Appl	c 808	11.8	42.1	53	4	US-09-072-596-200	Sequenc
42.1	27	3	US-08-759-306-584	Sequence 584, App	c 809	11.8	42.1	53	4	US-09-072-596-146	Sequenc
42.1	27	3	US-08-985-162-1395	Sequence 1395, Ap	c 810	11.8	42.1	53	4	US-09-072-967-205	Sequenc
42.1	27	4	US-08-584-040-480	Sequence 480, App	c 811	11.8	42.1	54	1	US-08-094-948A-3	Sequenc
42.1	27	4	US-08-584-040-1150	Sequence 1150, Ap	c 812	11.8	42.1	54	4	US-08-956-171B-1763	Sequenc
42.1	27	4	US-08-584-040-3280	Sequence 3280, Ap	c 813	11.8	42.1	54	5	PCT-US96-0319-3	Sequenc
42.1	27	4	US-08-584-040-4836	Sequence 4836, Ap	c 814	11.8	42.1	57	4	US-09-097-055B-44	Sequenc
42.1	27	4	US-09-401-063-1395	Sequence 1395, Ap	c 815	11.8	42.1	57	4	US-09-097-055B-46	Sequenc
42.1	28	3	US-08-623-326-19	Sequence 19, Appl	c 816	11.8	42.1	57	4	US-09-097-055B-50	Sequenc
42.1	28	3	US-08-325-426B-6	Sequence 6, Appl	c 817	11.8	42.1	58	2	US-09-674-677-8	Sequenc
42.1	30	1	US-08-480-547A-20	Sequence 20, Appl	c 819	11.8	42.1	59	3	US-09-097-767A-3	Sequenc
42.1	30	1	US-08-250-847B-20	Sequence 20, Appl	c 820	11.8	42.1	59	3	US-09-202-976-5	Sequenc
42.1	30	1	US-08-186-229-23	Sequence 23, Appl	c 821	11.8	42.1	60	4	US-09-624-693A-23	Sequenc
42.1	30	2	US-08-470-124-23	Sequence 23, Appl	c 822	11.8	42.1	60	4	US-09-250-609-29	Sequenc
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42.1	30	2	US-08-476-176B-35	Sequence 35, Appl	c 824	11.8	42.1	60	4	US-09-180-245-74	Sequenc
42.1	30	3	US-08-859-998-393	Sequence 393, App	c 825	11.6	41.4	18	4	US-09-422-978-11132	Sequenc
42.1	30	3	US-08-464-410A-20	Sequence 20, Appl	c 826	11.6	41.4	20	1	US-07-703-421-9	Sequenc
42.1	30	3	US-08-127-721A-35	Sequence 35, Appl	c 827	11.6	41.4	20	1	US-08-008-006A-9	Sequenc
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41.4	22	4	US-07-974-409C-160	Sequence 160, App	C 907	11.6	41.4	36	5	PCT-US93-11198-247	Sequenc
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41.4	22	5	PCT-US93-00977-160	Sequence 160, App	C 909	11.6	41.4	37	3	US-09-262-773-75	Sequenc
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41.4	24	4	US-09-582-224A-1	Sequence 22, Appl	C 913	11.6	41.4	38	1	US-08-435-628-297	Sequenc
41.4	25	3	US-08-943-731-229	Sequence 229, App	C 914	11.6	41.4	38	1	US-08-435-628-2102	Sequenc
41.4	25	4	US-09-866-108A-3098	Sequence 3098, Ap	C 915	11.6	41.4	38	1	US-08-435-628-2344	Sequenc
41.4	25	4	US-09-866-108A-3107	Sequence 3107, Ap	C 916	11.6	41.4	38	3	US-09-156-828B-31	Sequenc
41.4	25	4	US-09-866-108A-11214	Sequence 11214, A	C 917	11.6	41.4	38	4	US-09-371-772B-9216	Sequenc
41.4	25	4	US-09-866-108A-11215	Sequence 11215, A	C 918	11.6	41.4	38	4	US-09-371-772B-9393	Sequenc
41.4	25	4	US-09-866-108A-11216	Sequence 11216, A	C 919	11.6	41.4	38	4	US-09-371-772B-13183	Sequenc
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41.4	25	4	US-09-866-108A-11219	Sequence 11219, A	C 922	11.6	41.4	40	1	US-07-844-297-4	Sequenc
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41.4	25	4	US-09-866-108A-11355	Sequence 11355, A	C 927	11.6	41.4	41	4	US-09-042-492D-26	Sequenc
41.4	25	4	US-09-866-108A-11356	Sequence 11356, A	C 928	11.6	41.4	41	4	US-08-913-612A-26	Sequenc
41.4	25	4	US-09-866-108A-11357	Sequence 11357, A	C 929	11.6	41.4	42	1	US-08-399-696-22	Sequenc
41.4	25	4	US-09-866-108A-11358	Sequence 11358, A	C 930	11.6	41.4	43	2	US-08-850-049-107	Sequenc
41.4	25	4	US-09-866-108A-11359	Sequence 11359, A	C 931	11.6	41.4	43	2	US-08-050-478-107	Sequenc
41.4	25	4	US-09-866-108A-11360	Sequence 11360, A	C 932	11.6	41.4	43	3	US-09-414-117-107	Sequenc
41.4	26	2	US-08-852-806-4	Sequence 4, Appli	C 933	11.6	41.4	43	3	US-09-678-437-107	Sequenc
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41.4	26	4	US-08-899-112B-15	Sequence 15, Appl	C 935	11.6	41.4	44	1	US-07-714-131C-248	Sequenc
41.4	27	1	US-08-758-306-1196	Sequence 1196, Ap	C 936	11.6	41.4	44	1	US-08-412-110-248	Sequenc
41.4	27	3	US-08-793-418-10	Sequence 10, Appl	C 937	11.6	41.4	44	1	US-08-409-442A-248	Sequenc
41.4	27	4	US-08-584-040-6561	Sequence 6561, Ap	C 938	11.6	41.4	44	2	US-08-469-609A-248	Sequenc
41.4	27	4	US-09-305-681-31	Sequence 31, Appl	C 939	11.6	41.4	44	3	US-09-091-058-19	Sequenc
41.4	28	4	US-09-050-739-124	Sequence 124, App	C 940	11.6	41.4	44	3	US-09-143-190-248	Sequenc
41.4	30	1	US-08-186-229-17	Sequence 17, Appl	C 941	11.6	41.4	44	5	PCT-US93-11725-5	Sequenc
41.4	30	2	US-08-470-124-17	Sequence 37, Appl	C 942	11.6	41.4	44	5	PCT-US93-11725-5	Sequenc
41.4	30	2	US-08-468-352-58	Sequence 38, Appl	C 943	11.6	41.4	45	3	US-09-315-886C-17	Sequenc
41.4	30	4	US-08-894-454-7	Sequence 7, Appli	C 944	11.6	41.4	47	3	US-09-438-016-1	Sequenc
41.4	31	3	US-09-232-468A-19	Sequence 19, Appl	C 945	11.6	41.4	47	4	US-09-641-638-710	Sequenc
41.4	31	4	US-09-784-984B-15	Sequence 15, Appl	C 946	11.6	41.4	47	4	US-09-422-978-1562	Sequenc
41.4	31	4	US-09-402-214-43	Sequence 43, Appl	C 947	11.6	41.4	47	4	US-09-422-978-2510	Sequenc
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41.4	36	1	US-08-411-796-247	Sequence 247, App	C 955	11.6	41.4	50	1	US-08-449-045C-23	Sequenc
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41.4	36	2	US-08-292-620A-1521	Sequence 1521, Ap	C 958	11.6	41.4	50	2	US-08-435-605A-36	Sequenc
41.4	36	2	US-08-595-684B-311	Sequence 311, App	C 959	11.6	41.4	50	3	US-08-906-517-55	Sequenc
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41.4	36	2	US-08-585-684B-1122	Sequence 1122, Ap	C 961	11.6	41.4	51	1	US-08-450-246-40	Sequenc
41.4	36	2	US-08-585-684B-1124	Sequence 1124, Ap	C 962	11.6	41.4	51	1	US-08-450-098-40	Sequenc
41.4	36	2	US-08-921-382-7	Sequence 7, Appli	C 963	11.6	41.4	51	1	US-08-451-233-40	Sequenc
41.4	36	2	US-08-921-382-11	Sequence 11, Appl	C 964	11.6	41.4	51	1	US-08-450-236-40	Sequenc
41.4	36	3	US-08-471-039-245	Sequence 245, App	C 965	11.6	41.4	51	1	US-08-235-403-40	Sequenc
41.4	36	3	US-08-471-039-247	Sequence 247, App	C 966	11.6	41.4	51	4	US-09-387-418A-3	Sequenc
41.4	36	3	US-08-071-845-906	Sequence 906, App	C 967	11.6	41.4	51	4	US-09-443-199C-487	Sequenc
41.4	36	3	US-08-071-845-1343	Sequence 1343, Ap	C 968	11.6	41.4	51	4	US-09-443-199C-488	Sequenc
41.4	36	3	US-08-071-845-1521	Sequence 1521, Ap	C 969	11.6	41.4	51	4	US-09-126-420A-27	Sequenc
41.4	36	3	US-09-038-073-311	Sequence 311, App	C 970	11.6	41.4	53	4	US-09-126-420A-27	Sequenc
41.4	36	3	US-09-038-073-352	Sequence 352, App	C 971	11.6	41.4	54	4	US-09-479-645A-165	Sequenc
41.4	36	3	US-09-038-073-1122	Sequence 1122, Ap	C 972	11.6	41.4	54	4	US-09-479-645A-196	Sequenc
41.4	36	3	US-09-038-073-1124	Sequence 1124, Ap	C 973	11.6	41.4	55	1	US-08-450-257-39	Sequenc
41.4	36	4	US-08-559-330-245	Sequence 245, App	C 974	11.6	41.4	55	1	US-08-450-246-39	Sequenc
41.4	36	4	US-08-559-330-247	Sequence 247, App	C 975	11.6	41.4	55	1	US-08-450-098-39	Sequenc

41.4 55 1 US-08-451-233-39 Sequence 39, Appl
 41.4 55 1 US-08-450-236-39 Sequence 39, Appl
 41.4 55 1 US-08-235-403-39 Sequence 39, Appl
 41.4 55 4 US-09-088-274-3 Sequence 3, Appl
 41.4 59 1 US-08-275-156-1 Sequence 1, Appl
 41.4 59 1 US-08-275-156-2 Sequence 2, Appl
 41.4 59 5 PCT-US95-03866-29 Sequence 29, Appl
 41.4 60 2 US-08-749-852-52 Sequence 52, Appl
 41.4 60 2 US-08-749-852-54 Sequence 54, Appl
 41.4 60 4 US-09-459-956-22 Sequence 22, Appl
 41.4 60 4 US-08-584-040-7291 Sequence 7291, Ap
 40.7 17 4 US-09-371-772B-3100 Sequence 3100, Ap
 40.7 17 1 US-08-758-306-1357 Sequence 1357, Ap
 40.7 18 3 US-08-665-259-40 Sequence 40, Appl
 40.7 18 3 US-08-762-500-40 Sequence 40, Appl
 40.7 18 3 US-09-339-993-24 Sequence 24, Appl
 40.7 18 4 US-09-423-744A-10 Sequence 10, Appl
 40.7 19 1 US-08-631-200-58 Sequence 58, Appl
 40.7 19 1 US-08-829-553-58 Sequence 58, Appl
 40.7 19 2 US-08-922-267A-58 Sequence 58, Appl
 40.7 19 2 US-08-936-707A-58 Sequence 58, Appl
 40.7 19 3 US-08-936-706A-58 Sequence 58, Appl
 40.7 19 3 US-09-248-203-58 Sequence 58, Appl
 40.7 19 3 US-09-406-071-58 Sequence 58, Appl

ALIGNMENTS

Application US/08325426B
 017535
 ORIGINATOR:
 : FU, Jianlin
 : TAN, Boon-Huan
 : YAP, Eu-Hian
 : CHAN, Yow-Cheong
 : TAN, Yin-Hwee
 INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
 INVENTION: (SINGAPORE STRAIN)
 SEQUENCES: 25
 DENCE ADDRESS:
 2E: NIXON and VANDERHYE PC
 8th FLOOR, 1100 NORTH GLEBE ROAD
 ARLINGTON
 VIRGINIA
 : USA
 : 201-4714
 READABLE FORM:
 TYPE: Floppy disk
 : IBM PC compatible
 CG SYSTEM: PC-DOS/MS-DOS
 3: Patent in Release #1.0, Version #1.25 (EPO)
 APPLICATION DATA:
 NION NUMBER: US/08/325,426B
 DATE: 16-DEC-1994
 FOR SEQ ID NO: 7:
 CHARACTERISTICS:
 29 base pairs
 nucleic acid
 NNESS: single
 TYPE: linear
 TYPE: DNA (genomic)
 -7
 57.1%; Score 16; DB 3; Length 29;
 79.2%; Pred. No. 4.4e+02;
 : Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 AGCATCATCTCTGTCAGGTCAGG 24
 ATCAGAATTCTCTGTCAGGTCAGG 25

RESULT 2

US-08-819-458A-14/c
 ; Sequence 14, Application US/08819458A
 ; Patent No. 5891669
 ; GENERAL INFORMATION:
 ; APPLICANT: Jensen, Ejner B.
 ; APPLICANT: Cherry, Joel
 ; APPLICANT: Elrod, Susan L.
 ; TITLE OF INVENTION: Methods For Producing Polypeptides
 ; TITLE OF INVENTION: In Respiratory-Deficient Cells
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5891669o No. 5891669disk of No. 5891669th A
 ; STREET: 405 Lexington Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: U.S.A.
 ; ZIP: 10174
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/819,458A
 ; FILING DATE: 17-MAR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 5215.000-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-819-458A-14
 Query Match 55.7%; Score 15.6; DB 2; Length 30;
 Best Local Similarity 81.8%; Pred. No. 6.5e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0.

QY 1 AGCATCATCTCTGTCAGGTCGA 22

Db 26 ATCGTCATCTCTGTCGTCGA 5

RESULT 3

US-09-206-059-71
 ; Sequence 71, Application US/09206059
 ; Patent No. 6201104
 ; GENERAL INFORMATION:
 ; APPLICANT: MacDonald, Nicholas
 ; APPLICANT: Sim, Kim Lee
 ; TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Pept
 ; TITLE OF INVENTION: Proteins and Methods of Use
 ; FILE REFERENCE: 05213-0370
 ; CURRENT APPLICATION NUMBER: US/09/206,059
 ; CURRENT FILING DATE: 1998-12-04
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 71
 ; LENGTH: 33
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

INATION: Description of Artificial Sequence: synthetic
INATION: binding peptides

54.3%; Score 15.2; DB 3; Length 33;
milarity 85.0%; Pred. No. 9.7e+02;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

GCATCATCCTCTGCATGCT 20
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13 Application US/09315886C
25063

INATION:
Khvorova, Anastasia
Yarus, Michael
ENTION: RNA Channels in Biological Membranes

ICE: UTC-03444
ICATION NUMBER: US/09/315,886C

NG DATE: 1999-05-20
ATION NUMBER: 60/086,492
DATE: 1998-05-22
Q ID NOS: 32
tentin Ver. 2.0

rtificial Sequence

INATION: Description of Artificial Sequence: SYNTHETIC
13

52.9%; Score 14.8; DB 3; Length 50;
milarity 46.2%; Pred. No. 1.5e+03;
Conservative 7; Mismatches 7; Indels 0; Gaps 0;

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UCUUAUUCUGUGCGUGGAGGUC 32

19/c
Application US/09262773
25451

INATION:
allinger, Dennis G.
ing, Wei
agner, Susanne

ENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
ENTION: SUSCEPTIBILITY GENE CHD1
CE: Myriad 3

ICATION NUMBER: US/09/262,773

NG DATE: 1999-03-04
Q ID NOS: 210
tentin Ver. 2.0

rimer
19

52.1%; Score 14.6; DB 3; Length 40;
milarity 81.6%; Pred. No. 1.8e+03;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 33 GCACCTGCCTCTACATGTCATCA 13

RESULT 6

US-07-988-194A-8/c
; Sequence 8, Application US/07988194A
; Patent No. 5359046

; GENERAL INFORMATION:

; APPLICANT: Capon, Daniel J.

; APPLICANT: Weiss, Arthur

; APPLICANT: Irving, Brian A.

; APPLICANT: Roberts, Margo R.

; APPLICANT: Zsebo, Krisztina

; TITLE OF INVENTION: Chimeric Chains for Receptor

; TITLE OF INVENTION: Associated Signal Transduction Pathways

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hobbach, Test, Albritton &

; ADDRESSEE: Herbert

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/07/988,194A

; FILING DATE: December 9, 1992

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Rowland, Bertram I.

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: A-55107-1 CELL-0051

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-781-1989

; TELEFAX: 415-398-3249

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-07-988-194A-8

Query Match 51.4%; Score 14.4; DB 1; Length 26;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0;

QY 5 TCATCCTCTGCATGTCAGTCAT 28

Db 25 TCACCTCTCTCAAGTCAGATCTT 2

RESULT 7

US-08-258-152-14/c

; Sequence 14, Application US/08258152

; Patent No. 5686279

; GENERAL INFORMATION:

; APPLICANT: FINER, MITCHELL H.

; APPLICANT: ROBERTS, MARGO R.

; APPLICANT: DULL, THOMAS J.

; APPLICANT: ZSEBO, KRISZTINA M.

; APPLICANT: QIN, LU

; TITLE OF INVENTION: METHOD FOR PRODUCTION OF HIGH TITER

; TITLE OF INVENTION: VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDI.

; TITLE OF INVENTION: OF MAMMALIAN CELLS

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

3E: CELL GENESYS, INC.
322 LAKESIDE DRIVE
FOSTER CITY
CALIFORNIA
: USA
4404
READABLE FORM:
TYPE: Floppy disk
R: IBM PC compatible
NG SYSTEM: PC-DOS/MS-DOS
E: PatentIn Release #1.0, Version #1.25
PLICATION DATA:
TION NUMBER: US/08/258,152
DATE: 10-JUN-1994
ICATION: 435
LICATION DATA:
TION NUMBER: US 08/076,299
DATE: 11-JUN-1993
AGENT INFORMATION:
KRUPEN, KAREN I.
ATION NUMBER: 34,647
TE/DOCKET NUMBER: CELL 13.1
ICATION INFORMATION:
NE: 415-358-9600 X131
: 415-349-7392
FOR SEQ ID NO: 14:
CHARACTERISTICS:
26 base pairs
nucleic acid
DNES: single
Y: linear
TYPE: DNA (genomic)
14
51.4%; Score 14.4; DB 1; Length 26;
imilarity 75.0%; Pred. No. 2e+03; 6; Indels 0; Gaps 0;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;
ICATCTCTGCATGTCAGTTCAT 28
|||||
ICACCTTCTCAAGTTCAGATCTT 2

-14/c
Application US/08076299A
334256
RMATION:
: FINER, MITCHELL H.
: ROBERTS, MARGO R.
: DULL, THOMAS J.
: ZSEBO, KRISTINA M.
: QIN, LU
INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
INVENTION: VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
SEQUENCES: 30
DENCE ADDRESS:
SE: CELL GENESYS, INC.
322 LAKESIDE DRIVE
FOSTER CITY
CALIFORNIA
: USA
4404
READABLE FORM:
TYPE: Floppy disk
R: IBM PC compatible
NG SYSTEM: PC-DOS/MS-DOS
E: PatentIn Release #1.0, Version #1.25
PLICATION DATA:
TION NUMBER: US/08/076,299A
DATE: 11-JUN-1993
ICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 13.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
TELEFAX: 415-349-7392
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-076-299A-14
Query Match 51.4%; Score 14.4; DB 2; Length 26;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0
QY 5 TCATCCTCTGCATGTCAGTTCAT 28
|||||
DB 25 TCACCTTCTCAAGTTCAGATCTT 2
|||||
RESULT 9
US-08-438-582-14/c
Sequence 14, Application US/08438582
Patent No. 5858740
GENERAL INFORMATION:
APPLICANT: FINER, MITCHELL H.
APPLICANT: ROBERTS, MARGO R.
APPLICANT: DULL, THOMAS J.
APPLICANT: ZSEBO, KRISTINA M.
APPLICANT: QIN, LU
TITLE OF INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
TITLE OF INVENTION: VIRUS AND HIGH EFFICIENCY RETROVIRAL MED
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: CELL GENESYS, INC.
STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,582
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,152
FILING DATE: 10-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,299
FILING DATE: 11-JUN-93
ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 13.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
TELEFAX: 415-349-7392
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

26 base pairs
nucleic acid
NESS: single
: linear
YPE: DNA (genomic)
4

51.4%; Score 14.4; DB 2; Length 26;
milarity 75.0%; Pred. No. 2e+03; 6; Indels 0; Gaps 0;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

TCATCTCTGTCATGGTCAGGTCAT 28
|||||
CACCTTCTTCAAGGTCAGATCTT 2

4/c
Application US/09266596
18187

RMATION:
FINER, MITCHELL H.
DULL, THOMAS J.
ZSEBO, KRISZTINA M.
COOKE, KEEGAN
FARSON, DEBORAH A.

INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
INVENTION: VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
INVENTION: OF MAMMALIAN CELLS
SEQUENCES: 48

ENCE ADDRESS:
E: CELL GENESYS, INC.
322 LAKESIDE DRIVE
OSTER CITY
CALIFORNIA
USA

404

SADABLE FORM:
YPE: Floppy disk
: IBM PC compatible
3 SYSTEM: PC-DOS/MS-DOS
: PatentIn Release #1.0, Version #1.25
PLICATION DATA:
ION NUMBER: US/09/266,596
ATE:

CATION:
ICATION DATA:
ION NUMBER: 08/517,488
ATE: 21-AUG-1995
ION NUMBER: US 08/258,152
ATE: 10-JUN-1994
ICATION DATA:
ION NUMBER: US 08/076,299
ATE: 11-JUN-1993
SENT INFORMATION:
RUPEN, KAREN I.
TION NUMBER: 34,647
E/DOCKET NUMBER: CELL 13.3
ICATION INFORMATION:
E: 415-358-9600 X131
415-349-7392
FOR SEQ ID NO: 14:
HARACTERISTICS:
26 base pairs
nucleic acid
NESS: single
: linear
YPE: DNA (genomic)
4

51.4%; Score 14.4; DB 3; Length 26;
milarity 75.0%; Pred. No. 2e+03; 6; Indels 0; Gaps 0;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TCATCTCTGTCATGGTCAGGTCAT 28
|||||
Db 25 TCACCTTCTTCAAGGTCAGATCTT 2

RESULT 11

US-08-479-737-8/c
; Sequence 8, Application US/08479737
; Patent No. 6319494
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J
; ; Weiss, Arthur A
; ; Irving, Brian A
; ; Roberts, Margo R
; ; Zsebo, Krisztina
; ; TITLE OF INVENTION: CHIMERIC CHAINS FOR RECEPTOR ASSOCIATE
; ; SIGNAL TRANSDUCTION PATHWAYS
; ; NUMBER OF SEQUENCES: 51
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: CELL GENESYS, INC.
; ; STREET: 322 Lakeside Drive
; ; CITY: Foster City
; ; STATE: California
; ; COUNTRY: USA
; ; ZIP: 94404
; ; COMPUTER READABLE FORM:
; ; MEDIUM TYPE: Floppy disk
; ; OPERATING SYSTEM: PC-DOS/MS-DOS
; ; SOFTWARE: PatentIn Release #1.0, Version #1.25
; ; CURRENT APPLICATION DATA: US/08/479,737
; ; FILING DATE: 07-Jun-1995
; ; CLASSIFICATION: <Unknown>
; ; PRIOR APPLICATION DATA:
; ; APPLICATION NUMBER: 08/238,405
; ; FILING DATE: 05-MAY-1994
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: Mandel, Saralynn
; ; REGISTRATION NUMBER: 31,853
; ; REFERENCE/DOCKET NUMBER: Cell 5.3
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: (415) 358-9600
; ; TELEFAX: (415) 358-0803
; ; INFORMATION FOR SEQ ID NO: 8:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 26 base pairs
; ; TYPE: nucleic acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: cDNA
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-479-737-8

Query Match 51.4%; Score 14.4; DB 4; Length 26;
Best Local Similarity 75.0%; Pred. No. 2e+03; 6; Indels 0;
Matches 18; Conservative 0; Mismatches 6; Indels 0;

QY 5 TCATCTCTGTCATGGTCAGGTCAT 28
|||||
Db 25 TCACCTTCTTCAAGGTCAGATCTT 2

RESULT 12

US-08-475-442A-8/c
; Sequence 8, Application US/08475442A
; Patent No. 6407221
; GENERAL INFORMATION:
; APPLICANT: CAPON, DANIEL J
; ; APPLICANT: WEISS, ARTHUR
; ; APPLICANT: IRVING, BRIAN A
; ; APPLICANT: ROBERTS, MARGO R

ZSEBO, KRISTINA
INVENTION: CHIMERIC CHAINS FOR
RECEPTOR-ASSOCIATED SIGNAL TRANSDUCTION PATHWAYS
SEQUENCES: 51
PENCE ADDRESS:
CELL GENESYS, INC.
322 LAKESIDE DRIVE
FOSTER CITY
CALIFORNIA
USA
1404

READABLE FORM:
TYPE: Floppy disk
t: IBM PC compatible
g SYSTEM: PC-DOS/MS-DOS
3: PatentIn Release #1.0, Version #1.25
PLICATION DATA:
TION NUMBER: US/08/475,442A
DATE: 06-JUN-1995

ICATION DATA:
TION NUMBER: US 08/238,405
DATE: 05-MAY-1994
ICATION DATA:
TION NUMBER: US 07/988,194
DATE: 09-DEC-1992
ICATION DATA:
TION NUMBER: US 07/627,643
DATE: 14-DEC-1990
ICATION DATA:
TION NUMBER: PCT/US91/09431
DATE: 12-DEC-1991
AGENT INFORMATION:
CRUPEN, KAREN I
TION NUMBER: 34,647
E/DOCKET NUMBER: CELLS.5
ICATION INFORMATION:
E: (415)358-9600X131
FOR SEQ ID NO: 8:
CHARACTERISTICS:
26 base pairs
nucleic acid
NESS: single
f: linear
TYPE: cDNA
-8

51.4%; Score 14.4; DB 4; Length 26;
Similarity 75.0%; Pred.No.2e+03; 6; Indels 0; Gaps 0;
Conservative 0; Mismatches 6; Indels 0;

TCATCCTCTGCATGTCAGGTGCAT 28
|||||
TCACCTTCTTCAAGTCAGATCTT 2

14/c
Application US/09944411
306604
FORMATION:
CANT: FINER, MITCHELL H.
DULL, THOMAS J.
ZSEBO, KRISTINA M.
COOKE, KEEGAN
FARSON, DEBORAH A.

OF INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
OF MAMMALIAN CELLS
R OF SEQUENCES: 48
SPONSOR ADDRESS:
ADDRESSEE: CELL GENESYS, INC.

STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,411
FILING DATE: 04-SEP-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/914,893
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/258,152
FILING DATE: 10-JUN-1994
APPLICATION NUMBER: US 08/076,299
FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 13.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
TELEFAX: 415-349-7392
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-944-411-14

Query Match 51.4%; Score 14.4; DB 4; Length 26;
Best Local Similarity 75.0%; Pred.No.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0.

Qy 5 TCATCCTCTGCATGTCAGGTGCAT 28
|||||
Db 25 TCACCTTCTTCAAGTCAGATCTT 2

RESULT 14
US-08-439-813-1
Sequence 1, Application US/08439813
Patent No. 5631133
GENERAL INFORMATION:
APPLICANT: HANAHAN, Douglas
APPLICANT: YAMAMOTO, Keith
APPLICANT: VIVENCO, Maria del Mar
TITLE OF INVENTION: A TRANSITION IN TRANSCRIPTIONAL ACTIVATI
TITLE OF INVENTION: INTRACELLULAR HORMONE RECEPTORS AT THE T
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

ION NUMBER: US/08/439,813
DATE: 12-MAY-1995
CATION: 435
GENT INFORMATION:
harrett-Wackowski, Eugenia
TION NUMBER: 37,330
E/DOCKET NUMBER: 02307E-059800
ICATION INFORMATION:
IE: 415/543-9600
415/543-5043
FOR SEQ ID NO: 1:
HARACTERISTICS:
42 base pairs
nucleic acid
NESS: single
: linear
YPE: DNA (genomic)

51.4%; Score 14.4; DB 1; Length 42;
milarity 75.0%; Pred. No. 2.2e+03;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

GCATCATCTCTGTCATGTCAGG 24
|||||
ACAICATGTTCTGCGTCGCCAGG 41

-1
pplication PC/TUS9605291A
RMATION:

THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
NVENTION: A TRANSITION IN TRANSCRIPTIONAL ACTIVATION BY
NVENTION: INTRACELLULAR HORMONE RECEPTORS AT THE TUMOR STAGE
NVENTION: OF DERMAL FIBROSARCOMA DEVELOPMENT
SEQUENCES: 3

ENCE ADDRESS:
E: Robbins, Berliner & Carson
201 N. Figueroa Street, 5th Floor
os Angeles
California
USA

012-2628
EADABLE FORM:
YPE: Floppy disk
: IBM PC compatible
G SYSTEM: PC-DOS/MS-DOS
: Patentin Release #1.0, Version #1.30
PLICATION DATA:
ION NUMBER: PCT/US96/05291A

ATE:
CATION:
GENT INFORMATION:
erliner, Robert
TION NUMBER: 20,121
E/DOCKET NUMBER: S555-382
ICATION INFORMATION:
IE: 213-977-1001
213-977-1003
FOR SEQ ID NO: 1:
HARACTERISTICS:
42 base pairs
nucleic acid
NESS: single
: linear
YPE: DNA (genomic)

-1
51.4%; Score 14.4; DB 5; Length 42;
milarity 75.0%; Pred. No. 2.2e+03;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AGCATCATCTCTGTCATGTCAGG 24
Db 18 AACATCATGTTCTGCGTCGCCAGG 41
RESULT 16
US-09-383-143-20
; Sequence 20, Application US/09383143
; Patent No. 6372429
; GENERAL INFORMATION:
; APPLICANT: SHARON, GIL
; TITLE OF INVENTION: METHOD FOR ASSEMBLY OF MULTIPLE DNA FRAGMENT
; FILE REFERENCE: LUZZATTO 3.3-061 CONT
; CURRENT APPLICATION NUMBER: US/09/383,143
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/IL98/00096
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule: P
US-09-383-143-20

Query Match 51.4%; Score 14.4; DB 4; Length 47;
Best Local Similarity 54.2%; Pred. No. 2.2e+03;
Matches 13; Conservative 5; Mismatches 6; Indels 0;

Qy 1 AGCATCATCTCTGTCATGTCAGG 24
Db 2 AUCAUCAUCAUCAUCAUCAUG 25

RESULT 17
US-09-158-863C-43/c
; Sequence 43, Application US/09158863C
; Patent No. 6280978
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Lloyd G.
; APPLICANT: Garcia-Blanco, Mariano A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
; FILE REFERENCE: 31304-B-A
; CURRENT APPLICATION NUMBER: US/09/158,863C
; CURRENT FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 09/133,717
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 09/087,233
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 08/766,354
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: 60/008,317
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-158-863C-43

Query Match 51.4%; Score 14.4; DB 3; Length 51;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0;

Qy 1 AGCATCATCTCTGTCATGTCAGG 24
Db 35 AGCATCATCATCATCATCATG 12

10 Application US/08687865A
 55596
 INFORMATION:
 Jones, Kevin F.
 Zagursky, Robert J.
 Cui, Peggy
 INVENTION: The NuCa Protein of Haemophilus
 INVENTION: influenzae and the Gene Encoding That Protein
 SEQUENCES: 23
 SEQUENCE ADDRESS:
 BE: American Cyanamid Company
 One Cyanamid Plaza
 Wayne
 New Jersey
 U.S.A.
 7470
 READABLE FORM:
 TYPE: Floppy disk
 R: IBM PC compatible
 G SYSTEM: PC-DOS/MS-DOS
 3: PatentIn Release #1.0, Version #1.30
 APPLICATION DATA:
 ION NUMBER: US/08/687,865A
 DATE: 26-JUL-1996
 CATION: 536
 GENT INFORMATION:
 Jordon, Alan M.
 ATION NUMBER: 30,637
 E/DOCKET NUMBER: 33,250-00
 ICAION INFORMATION:
 HE: 201-831-3244
 : 201-831-3305
 FOR SEQ ID NO: 10:
 53 base pairs
 nucleic acid
 NNESS: single
 f: linear
 TYPE: DNA (genomic)
 -10
 51.4%; Score 14.4; DB 2; Length 53;
 Similarity 75.0%; Pred. No. 2.2e+03;
 ; Conservative 0; Mismatches 6; Indels 0;
 AGCATCATCTCTGCATGGTCAGG 24
 |||||
 ATCATCATCATCATCATGGTATGG 53
 10 Application US/09043711
 221365
 INFORMATION:
 Jones, Kevin F.
 Zagursky, Robert J.
 Cui, Peggy
 INVENTION: The NuCa Protein of Haemophilus
 INVENTION: influenzae and the Gene Encoding That Protein
 SEQUENCES: 23
 SEQUENCE ADDRESS:
 BE: American Cyanamid Company
 One Cyanamid Plaza
 Wayne
 New Jersey
 U.S.A.
 7470
 READABLE FORM:
 TYPE: Floppy disk
 R: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/043,711
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/687,865
 FILING DATE: 26-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Gordon, Alan M.
 REGISTRATION NUMBER: 30,637
 REFERENCE/DOCKET NUMBER: 33,250-00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-831-3244
 TELEFAX: 201-831-3305
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 53 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-043-711-10
 Query Match 51.4%; Score 14.4; DB 3; Length 53;
 Best Local Similarity 75.0%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0,
 Qy 1 AGCATCATCTCTGCATGGTCAGG 24
 |||||
 Db 30 ATCATCATCATCATCATGGTATGG 53
 RESULT 20
 US-08-687-865A-11/c
 ; Sequence 11, Application US/08687865A
 ; Patent No. 5955596
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Kevin F.
 ; APPLICANT: Zagursky, Robert J.
 ; APPLICANT: Cui, Peggy
 ; TITLE OF INVENTION: The NuCa Protein of Haemophilus
 ; TITLE OF INVENTION: influenzae and the Gene Encoding That Pro
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: American Cyanamid Company
 ; STREET: One Cyanamid Plaza
 ; CITY: Wayne
 ; STATE: New Jersey
 ; COUNTRY: U.S.A.
 ; ZIP: 07470
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/687,865A
 ; FILING DATE: 26-JUL-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gordon, Alan M.
 ; REGISTRATION NUMBER: 30,637
 ; REFERENCE/DOCKET NUMBER: 33,250-00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-831-3244
 ; TELEFAX: 201-831-3305
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 55 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

3 09:04:21 2004

us-10-090-326-23.max.rni

```
: linear
YPE: DNA (genomic)
11
51.4%; Score 14.4; DB 2; Length 55;
milarity 75.0%; Pred. No. 2.3e+03;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

GCATCATCCTCTGCATGTCAGG 24
||||| ||| ||||| ||
TCATCATCATCATCATGTTATGG 5

1/c
Application US/09043711
21365
RMATION: Jones, Kevin F.
Zagursky, Robert J.
Coi, Peggy
NVENTION: The NuCA Protein of Haemophilus
NVENTION: Influenzae and the Gene Encoding That Protein
SEQUENCES: 23
ENCE ADDRESS:
E: American Cyanamid Company
One Cyanamid Plaza
ayne
New Jersey
U.S.A.
470
EADABLE FORM:
YPE: Floppy disk
: IBM PC compatible
G SYSTEM: PC-DOS/MS-DOS
: PatentIn Release #1.0, Version #1.30
PLICATION DATA:
ION NUMBER: US/09/043,711
ATE:
ICATION:
ION DATA:
ION NUMBER: US 08/587,865
ATE: 26-JUL-1996
GENT INFORMATION:
ordon, Alan M.
TION NUMBER: 30,637
E/DOCKET NUMBER: 33,250-00
ICATION INFORMATION:
E: 201-831-3244
201-831-3305
FOR SEQ ID NO: 11:
HARACTERISTICS:
55 base pairs
ucleic acid
NESS: single
: linear
YPE: DNA (genomic)
1
51.4%; Score 14.4; DB 3; Length 55;
milarity 75.0%; Pred. No. 2.3e+03;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

GCATCATCCTCTGCATGTCAGG 24
||||| ||| ||||| ||
TCATCATCATCATCATGTTATGG 5

3
Application US/09490692
80353
MATION:
: APPLICANT: Nicholas M. Dean
: APPLICANT: Lex M. Cowseirt
: TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
: FILE REFERENCE: RTS-0120
: CURRENT APPLICATION NUMBER: US/09/490,692
: CURRENT FILING DATE: 2000-01-24
: NUMBER OF SEQ ID NOS: 176
: SEQ ID NO 13
: LENGTH: 29
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: PCR Probe
US-09-490-692-13

Query Match 50.7%; Score 14.2; DB 3; Length 29;
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0;

Qy 2 GCATCATCCTCTGCATGGT 20
||| ||||| ||| |||
Db 7 GCAACATCCTCTCCAGGT 25

RESULT 23
US-09-144-428-61/c
; Sequence 61, Application US/09144428
; Patent No. 6583108
; GENERAL INFORMATION:
; APPLICANT: BAYER CORPORATION, The
; APPLICANT: TAMBURINI, Paul P
; APPLICANT: DAVIS, Gary
; APPLICANT: DELARIA, Katherine A
; APPLICANT: MARLOR, Christopher W
; APPLICANT: MULLER, Daniel K
; TITLE OF INVENTION: HUMAN BIKUNIN
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive Suite 3200
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,428
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/03894
; FILING DATE: 10-MAR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,106
; FILING DATE: 11-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,793
; FILING DATE: 14-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/725,251
; FILING DATE: 04-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAO, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 96,223-II
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 913-0001
; TELEFAX: (312) 913-0002
```

us-10-090-326-23.max.rni

```

; Patent No. 591411C
;
; GENERAL INFORMATION:
;
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
;

```

/ CORRESPONDENCE ADDRESS:
 / ADDRESS: SmithKline Beecham Corp./Corporate
 / ADDRESS: Intellectual Property
 / ADDRESS: Intellectual Property
 / STREET: P.O. Box 1539 / UW2220
 / CITY: King of Prussia
 / STATE: PA

STATE: PA
COUNTRY: USA
ZIP: 19406-0939

```

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483.636
;

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APPLICATION NUMBER: US/08/483,63
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA: US 08/136783
APPLICATION NUMBER: 14-OCT-1993
FILING DATE:

FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994

FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34, 028
REFERENCE/DOCKET NUMBER: P50186-3

REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090

TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

```

; ;
; ;
; ;
; ;

```

SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid

```

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown

```

```
:  
:  
: TOPOLOGY: unknown  
:  
: MOLECULE TYPE: cdna  
:  
: FEATURE:
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FEATURE:
NAME/KEY: CDS
LOCATION: 1..57

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LOCATION: 1..57
US-08-483-636-7

Query Match	Score 1
Best Local Similarity	50.7%;
	84.2%; Pred. N

Best Local Similarity 84.2%; Pred. N
Matches 16; Conservative 0; Mism

QY 2 GCATCATCCTCTGCATGGT 20

Db 14 GTATCATCCTCTTCTGGT 32

RESULT 26
US-08-483-632-7
Sequence 7 Application US/08483632

Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.

APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.

TITLE OF INVENTION:	Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION:	Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES:	75

NUMBER OF SEQUENCES: 75

09:04:21 2004

us-10-090-326-23.max.rni

NCE ADDRESS:
: SmithKline Beecham Corp./Corporate
: Intellectual Property
: P.O. Box 1539 / UW2220
: rg of Prussia
: A
: USA
06-0939
ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
LICATON DATA:
ON NUMBER: US/08/483,632
TE:
ATION:
CATION DATA:
ON NUMBER: US 08/117366
TE: 07-SEP-1993
CATION DATA:
ON NUMBER: US 08/136783
TE: 14-OCT-1993
CATION DATA:
ON NUMBER: PCT/US/94/10308
TE: 07-SEP-1994
ENT INFORMATION:
enton, Jeffrey A.
ON NUMBER: 34,028
/DOCKET NUMBER: P50186-3
CATION INFORMATION:
: (215) 270-5024
OR SEQ ID NO: 7:
CHARACTERISTICS:
57 base pairs
iclic acid
ESS: double
unknown
PE: CDNA
CDS
1..57
50.7%; Score 14.2; DB 2; Length 57;
ilarity 84.2%; Pred. No. 2.8e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;
ATCATCCTCTGCGATGGT 20
ATCATCCTCTCTCTGGT 32
5/c
pplication US/08454899G
2503
ATION:
abb, Roy R.
arr, Frank J.
tempest, Philip R.
ENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
E: 10274-007001
ICATION NUMBER: US/08/454,899G
NG DATE: 1995-05-31
ATION NUMBER: US 08/004,798
DATE: 1993-01-12
ATION NUMBER: PCT/US94/00266
DATE: 1994-01-07
ID NOS: 109
stSEQ for Windows Version 4.0

: LENGTH: 57
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: oligonucleotide for vector construction
US-08-454-899G-95
Query Match 50.7%; Score 14.2; DB 4; Length 57;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0;
Qy 2 GCATCATCCTCTGCGATGGT 20
Db 40 GCATCATCCTCTCTCTGGT 22
RESULT 28
US-09-158-863C-35/c
: Sequence 35, Application US/09158863C
: Patent No. 6280978
: GENERAL INFORMATION:
: APPLICANT: Mitchell, Lloyd G.
: APPLICANT: Garcia-Blanco, Mariano A.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
: TITLE OF INVENTION: SPLICEOSOME MEDIATED RNA TRANS-SPLICING
: FILE REFERENCE: 31304-B-A
: CURRENT APPLICATION NUMBER: US/09/158,863C
: CURRENT FILING DATE: 1998-09-23
: PRIOR APPLICATION NUMBER: 09/133,717
: PRIOR FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: 09/087,233
: PRIOR FILING DATE: 1998-05-28
: PRIOR APPLICATION NUMBER: 08/766,354
: PRIOR FILING DATE: 1996-12-13
: PRIOR APPLICATION NUMBER: 60/008,317
: PRIOR FILING DATE: 1995-12-07
: NUMBER OF SEQ ID NOS: 68
: SOFTWARE: FastSEQ for Windows Version 3.0
: SEQ ID NO 35
: LENGTH: 35
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Oligonucleotide primers complimentary to beta
: OTHER INFORMATION: gene (accession #X00266)
US-09-158-863C-35
Query Match 50.0%; Score 14; DB 3; Length 35;
Best Local Similarity 77.3%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0;
Qy 1 AGCATCATCCTCTGCGATGGTCA 22
Db 28 AGCAGCAGCCCTCGCAGGGTTA 7
RESULT 29
US-08-428-370A-1/c
: Sequence 1, Application US/08428370A
: Patent No. 5569583
: GENERAL INFORMATION:
: APPLICANT: Greenberg, Steven J.
: APPLICANT: Evans, Mary Jo
: TITLE OF INVENTION: Rapid and Sensitive Detection of
: TITLE OF INVENTION: Herpesviruses
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
: STREET: 1800 One M&T Plaza
: CITY: Buffalo
: STATE: New York
: COUNTRY: United States
: ZIP: 14203-2391

us-10-090-326-23.max.rni

```

; TELEFAX: 716-849-0349
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Cytomegalovirus
; FEATURE:
; LOCATION: GenBank locus HSSMIEG
US-08-600-764-1

Query Match 50.0%; Score 14; DB 2; Length 38;
Best Local Similarity 77.3%; Pred.No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0;

QY 6 CATCCTCTGCATGGTCAGGTCA 27
    ||| ||||| ||| |||
Ddb 33 CATGCTCTGCATAGTAGCCCA 12

RESULT 31
US-09-517-467B-294
; Sequence 294, Application US/09517467B
; Patent No. 6451602
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Ilex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION
; FILE REFERENCE: RTS-0150
; CURRENT APPLICATION NUMBER: US/09/517,467B
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/517,467
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 345
; SEQ ID NO 294
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-467B-294

Query Match 49.3%; Score 13.8; DB 4; Length 20;
Best Local Similarity 88.2%; Pred.No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 2 GCATCATCCTCTGCATG 18
    ||| ||||| ||| |||
Ddb 2 GCCTCATCCTCTGCCTG 18

RESULT 32
US-08-777-405A-7/c
; Sequence 7, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoeckstra, Merl F.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; SYSTEM: PC-DOS/MS-DOS
; PatentIn Release #1.0, Version #1.30
PLICATION DATA:
ION NUMBER: US/08/777,405A
ATE:

CATION: 435
ENT INFORMATION:
o. 5882910and, Greta E.
ION NUMBER: 35,302
E/DOCKET NUMBER: 27866/33441
ICATION INFORMATION:
2: (312) 474-6300
2: (312) 474-0448
25-3856

FOR SEQ ID NO: 7:
HARACTERISTICS:
21 base pairs
ucleic acid
NESS: single
YPE: other nucleic acid
7

49.3%; Score 13.8; DB 2; Length 21;
milarity 88.2%; Pred. No. 3.5e+03; Indels 0; Gaps 0;
Conservative 0; Mismatches 2; Indels 0;

PCCTCTGCATGCTCAG 23
|||||
TCATCTGCAGGGTCAG 5

7/c
plication US/08977871A
82910

EMATION:
Chantry, David
Hoekstra, Merl F.
Holtzman, Douglas A
NVENTION: No. 5882910el Lipid Kinase
SEQUENCES: 17
ENCE ADDRESS:
3: Marshall O'Toole Gerstein Murray & Borun
6300 Sears Tower/233 South Wacker Drive
chicago
Illinois
USA

506
SADABLE FORM:
YPE: Floppy disk
; IBM PC compatible
3 SYSTEM: PC-DOS/MS-DOS
; PatentIn Release #1.0, Version #1.30
PLICATION DATA:
ION NUMBER: US/08/977,871A
ATE:

CATION:
ICATION DATA:
ION NUMBER: 08/777,405
ATE:

GENT INFORMATION:
o. 5882910and, Greta E.
TION NUMBER: 35,302
E/DOCKET NUMBER: 27866/33441
ICATION INFORMATION:
E: (312) 474-6300
2: (312) 474-0448
25-3856

FOR SEQ ID NO: 7:
HARACTERISTICS:
21 base pairs
ucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-977-871A-7

Query Match 49.3%; Score 13.8; DB 2; Length 21;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 7 ATCCTCTGCATGCTCAG 23
|||||
Db 21 ATCACTGCAGGGTCAG 5

RESULT 34

US-09-225-951-7/c
; Sequence 7, Application US/09225951
; Patent No. 5985589
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5985589el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,951
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985589and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-09-225-951-7

Query Match 49.3%; Score 13.8; DB 2; Length 21;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 7 ATCCTCTGCATGCTCAG 23
|||||
Db 21 ATCACTGCAGGGTCAG 5

RESULT 35

US-09-253-396A-67/c
; Sequence 67, Application US/09253396A
; Patent No. 6205404
; GENERAL INFORMATION:
; APPLICANT: Genome Dynamics, Inc.
; TITLE OF INVENTION: DNA-Binding Proteins of the Zinc-Finger Cla

JE: 1116242-0003 file: genome03F.app
LOCATION NUMBER: US/09/253,396A
G DATE: 1999-02-19
ID NOS: 231
acntin ver. 2.0

accharomyces cerevisiae

67

49.3%; Score 13.8; DB 3; Length 27;
ilarity 88.2%; Pred. No. 3.7e+03;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TCATCCTCTGCATGGT 20
|||||
TCATCCTGGGCAATGGT 11

31 Application US/08646789A

22863

RMATION:

Peyman, John A.

INVENTION: REGULATION OF GENE EXPRESSION

SEQUENCES: 101

ENCE ADDRESS:

E: PENNIE & EDMONDS

1155 Avenue of the Americas

ew York

New York

U.S.A.

036-2711

ADABLE FORM:

YPE: Floppy disk

: IBM PC compatible

G SYSTEM: PC-DOS/MS-DOS

: Patentin Release #1.0, Version #1.30

PLICATION DATA:

ION NUMBER: US/08/646,789A

ATE: May 21, 1996

ICATION: 800

AGENT INFORMATION:

isrock, S. Leslie

ATION NUMBER: 18,872

ZE/DOCKET NUMBER: 6523-006

ICATION INFORMATION:

JE: (212) 790-9090

(212) 869-9741/8864

66141 PENNIE

FOR SEQ ID NO: 31:

CHARACTERISTICS:

29 base pairs

nucleic acid

NESS: single

f: linear

TYPE: DNA

-31

49.3%; Score 13.8; DB 3; Length 29;
ilarity 72.0%; Pred. No. 3.7e+03;
Conservative 0; Mismatches 7; Indels 0; Gaps 0;

ATCATCCTCTGCATGGTCAAT 28

|||||

ATGTTGCTCTGATGTAAGAAT 27

-23

Application US/09354231B

; Patent No. 6342658
; GENERAL INFORMATION:
; APPLICANT: DeBonte, Lorin R.
; APPLICANT: Shorosh, Basil S.
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES
; FILE REFERENCE: 07148-063002
; CURRENT APPLICATION NUMBER: US/09/354,231B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 08/874,109
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-354-231B-23

Query Match 49.3%; Score 13.8; DB 4; Length 32;
Best Local Similarity 60.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 3; Mismatches 7; Indels 0;

QY 1 AGCATCATCCTCTGCATGGTCAAGT 25

Db 2 AUCAUCAUCAUCITCTTCGTAGGGT 26

RESULT 38

US-09-128-602B-23

; Sequence 23, Application US/09128602B

; Patent No. 6414223

; GENERAL INFORMATION:

; APPLICANT: Kodali, Dharna

; APPLICANT: Fan, Zhegong

; APPLICANT: DeBonte, Lorin R.

; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TC

; FILE REFERENCE: 07148-072001

; CURRENT APPLICATION NUMBER: US/09/128,602B

; CURRENT FILING DATE: 1998-08-03

; NUMBER OF SEQ ID NOS: 68

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 23

; LENGTH: 32

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-09-128-602B-23

Query Match 49.3%; Score 13.8; DB 4; Length 32;
Best Local Similarity 60.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 3; Mismatches 7; Indels 0;

QY 1 AGCATCATCCTCTGCATGGTCAAGT 25

Db 2 AUCAUCAUCAUCITCTTCGTAGGGT 26

RESULT 39

US-09-995-297-23

; Sequence 23, Application US/09995297

; Patent No. 6649782

; GENERAL INFORMATION:

; APPLICANT: Kodali, Dharna

; APPLICANT: Fan, Zhegong

; APPLICANT: DeBonte, Lorin R.

; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TC

; FILE REFERENCE: 07148-072002

; CURRENT APPLICATION NUMBER: US/09/995,297

09:04:21 2004

us-10-090-326-23.max.rni

NG DATE: 2001-11-27
ATION NUMBER: US 09/128,602
DATE: 1998-08-03
ID NOS: 68
stSEQ for Windows Version 4.0

rtificial Sequence

ATION: primer

49.3%; Score 13.8; DB 4; Length 32;
ilarity 60.0%; Pred. No. 3.7e+03;
Conservative 3; Mismatches 7; Indels 0; Gaps 0;

3CATCATCTCTGTCAGGT 25

JCAUCAUCAUCTTCTCGTAGGT 26

pplication US/08439585

07831

RMATION:

Apeler, Heiner; Beinink, Jorgen;

Dorschug, Michael; Gottschalk, Uwe

VENTION: PROCESS FOR PREPARING AND RECOMBINANT

VENTION: RECOMBINANT APROTININ AND RECOMBINANT

VENTION: APROTININ VARIANTS HAVING THE NATURAL N-

VENTION: TERMINAL SEQUENCE

SEQUENCES: 4

ENCE ADDRESS:

S. SPRUNG HORN KRAMER & WOODS

660 White Plains Road

arrytown

New York

U.S.A.

591-5144

ADABLE FORM:

YPE: Diskette, 3.50 inch, 1.44MB

YPE: storage

: NEC Powermate SX/20

G SYSTEM: DOS

: Wordperfect 5.1

PLICATION DATA:

ION NUMBER: US/08/439,585

ATE: 11-MAY-1995

CATION: 435

ICATION DATA:

ION NUMBER: P 44 17 353.9 (Germany)

ATE: 18-MAY-1994

GENT INFORMATION:

urt G. Briscoe

TION NUMBER: 33,141

E/DOCKET NUMBER: Bayer 9285-KGB

ICATION INFORMATION:

E: (914) 332-1700

(914) 332-1844

FOR SEQ ID NO: 1:

CHARACTERISTICS:

42 base pairs

nucleic acid

NESS: single

: linear

YPE: DNA (genomic)

AL: no

: no

Query Match 49.3%; Score 13.8; DB 1; Length 42;
Best Local Similarity 72.0%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0;

QY 2 GCATCATCTCTGTCAGGT 26

Db 1 GCAGCATCTCTCGATTAGCTGTC 25

Search completed: April 12, 2004, 19:17:31

Job time : 113.179 secs

09:04:21 2004

us-10-090-326-23.max.rng

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

April 12, 2004, 14:34:57 ; Search time 109.077 Seconds
(without alignments)
1090.511 Million cell updates/sec

US-10-090-326-23

1 agcatcatctctgcagtgcat 28

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

3373863 seqs, 2124099041 residues

hits satisfying chosen parameters: 3308108

length: 0
length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002as:*

7: Geneseq2003as:*

8: Geneseq2003bs:*

9: Geneseq2003cs:*

10: Geneseq2004s:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
100.0	28	6	ABQ82557	Internal	Abq82557 Internal
71.4	20	2	AAV84287	LacZ repo	AAV84287 LacZ repo
71.4	20	6	ABT08197	Recombina	Abt08197 Recombina
71.4	20	9	ADB81355	PCR prime	ADB81355 PCR prime
67.9	19	2	AAV82445	LacZ gene	AAV82445 LacZ gene
64.3	30	2	AAV23280	H. vulgar	AAV23280 H. vulgar
62.1	30	6	ABN50202	Human spl	Abn50202 Human spl
61.4	40	6	ABT12156	E coli ex	Abt12156 E coli ex
60.7	40	6	ABT12155	E coli ex	Abt12155 E coli ex
60.0	60	6	ABN48389	Human spl	Abn48389 Human spl
57.1	29	2	AAQ51481	Dengue vi	AAQ51481 Dengue vi
57.1	42	2	AAV39800	Oligonuc	AAV39800 Oligonuc
55.7	30	2	AAV45436	Aspergill	AAV45436 Aspergill
55.0	60	6	ABN39943	Human spl	Abn39943 Human spl
55.0	60	6	ABN37161	Human spl	Abn37161 Human spl
54.3	33	3	AA68232	Angiogene	AA68232 Angiogene
54.3	39	5	AAV75700	Human GAD	AAV75700 Human GAD
54.3	56	2	AAV20388	Primer 5	AAV20388 Primer 5
54.3	58	6	AAI72186	Primer CD	AAI72186 Primer CD
54.3	60	6	ABN47436	Human spl	Abn47436 Human spl
53.6	25	8	ACI09245	Human mic	ACI09245 Human mic
53.6	41	6	AAE88866	Aldehyde/	AAE88866 Aldehyde/
53.6	44	4	AAH43442	Primer J	AAH43442 Primer J

Abn58990	60	6	ABN58990
Abn59110	60	6	ABN59110
Ac119518	25	8	ACI19518
Aaa79182	31	3	AAA79182
Aaz47149	50	3	AZA47149
Abz01817	50	6	ABZ01817
Abz04312	51	4	AAI74312
Acad15508	53	7	ACA15508
Abn45948	60	6	ABN45948
Abn43493	60	6	ABN43493
AcD20446	22	7	ACD20446
AcD20449	22	7	ACD20449
Ac100102	25	8	ACI00102
Ac100103	25	8	ACI00103
AAV46380	30	2	AAV46380
Abz81394	34	7	ABZ81394
Abz81393	34	7	ABZ81393
Aaz26944	40	2	AZ26944
Aas12817	45	4	AAS12817
Aas12808	46	4	AAS12808
Ab100335	51	5	ABL00335
Abn33282	60	6	ABN33282
Abn46151	60	6	ABN46151
Abn00919	20	7	ABA00919
ACK09538	25	8	ACK09538
AC190733	25	8	ACI90733
AAQ74319	26	2	AAQ74319
AAQ76230	26	2	AAQ76230
AAV05347	26	2	AAV05347
AAV97354	26	2	AAV97354
AAV68122	26	2	AAV68122
AAV99472	26	2	AAV99472
Aas17773	26	2	AAS17773
ABQ78242	26	6	ABQ78242
ABX64358	26	6	ABX64358
Abx10446	26	7	ABX10446
Aaq32739	34	2	AAQ32739
AB155973	34	6	ABL55973
ABZ45318	41	6	ABZ45318
ABZ46763	41	6	ABZ46763
AAV1570	42	2	AAV1570
AAV58140	42	2	AAV58140
Aaz99400	51	3	AAZ99400
ABQ73461	51	6	ABQ73461
ADD28176	51	9	ADD28176
AAH43142	54	5	AAH43142
ABN36233	60	6	ABN36233
AAI71414	22	4	AAI71414
AAV60738	22	2	AAV60738
ACI46046	25	8	ACI46046
AAf72912	29	4	AAf72912
Abz24840	30	7	ABZ24840
Aaz50971	34	3	AAZ50971
Aad06561	44	4	AAD06561
AAa70390	45	3	AAA70390
AAQ91390	51	2	AAQ91390
Aat48748	51	2	AAT48748
AAI75896	51	4	AAI75896
AAH79852	51	4	AAH79852
AAQ69928	57	2	AAQ69928
AAc02410	57	2	AAc02410
AAQ83495	57	2	AAQ83495
AAV79534	57	2	AAV79534
AAH97070	60	6	AAH97070
Abn35226	60	6	ABN35226
Abn42541	60	6	ABN42541
Abn45310	60	6	ABN45310
Abn41654	60	6	ABN41654
AA160485	60	7	AA160485
AAT33210	25	2	AAT33210
AAS12153	25	4	AAS12153
ADA74773	25	8	ADA74773
ABV75985	27	7	ABV75985

50.0	29	2	AAV44876	Aav44876 Probe for	c 170	13.8	49.3	52	6	AA138810
50.0	29	5	AAf98550	Aaf98550 Human cDN	c 171	13.8	49.3	52	6	ABK46276
50.0	30	2	Aaz09724	Aaz09724 S. cerevi	c 172	13.8	49.3	52	6	ABK46316
50.0	30	6	ABa81781	Abas81781 PCR prime	c 173	13.8	49.3	53	6	ABL58495
50.0	31	6	ABQ76912	Abq76912 hdm2 prot	c 174	13.8	49.3	54	3	AAa73940
50.0	32	3	AAV55524	Aav55524 G-CSF cat	c 175	13.8	49.3	55	7	ABV99721
50.0	35	3	AAZ99392	Aaz99392 PCR prime	c 176	13.8	49.3	55	3	AAZ96977
50.0	35	6	ABQ73453	Abq73453 Human bet	c 177	13.8	49.3	60	6	ABK15020
50.0	35	6	ABQ73481	Abq73481 Human bet	c 178	13.8	49.3	60	6	ABN39954
50.0	38	2	AA747983	Aat747983 Cytomegal	c 179	13.8	49.3	60	6	ABN32494
50.0	38	2	AAV72563	Aav72563 Cytomegal	c 180	13.8	49.3	60	6	ABN37758
50.0	39	6	ABSG61182	ABSG61182 Human pol	c 181	13.8	49.3	60	6	ABN33459
50.0	41	7	ABX75270	ABX75270 Human gen	c 182	13.8	49.3	60	6	ABN38311
50.0	47	4	AAH88415	Aah88415 CNS disor	c 183	13.8	49.3	60	6	ABN43288
50.0	50	6	AAAL45416	Aal45416 Cobalt-de	c 184	13.6	48.6	20	7	ABK88103
50.0	51	3	AAZ29333	Aaz29333 Primer 2	c 185	13.6	48.6	20	7	ABZ77225
50.0	51	4	AAI78261	Aai78261 Human sil	c 186	13.6	48.6	21	6	AAAD31429
50.0	51	4	AAI78260	Aai78260 Human sil	c 187	13.6	48.6	21	6	AAAX06595
50.0	51	5	ABL00695	ABL00695 Human sil	c 188	13.6	48.6	23	2	AAAF76641
50.0	52	4	AAH36992	Aah36992 Human col	c 189	13.6	48.6	24	2	AAAX84498
50.0	55	3	AAAG0852	Aag0852 AS-DHFR-G	c 190	13.6	48.6	24	7	ADA68190
50.0	55	3	AAAG0851	Aag0851 AS-DHFR-G	c 191	13.6	48.6	25	4	AAF77678
50.0	60	2	AAZ09720	Aaz09720 S. cerevi	c 192	13.6	48.6	25	6	ABN03112
50.0	60	2	AAAG0853	Aag0853 AS-DHFR-G	c 193	13.6	48.6	25	6	ABN03113
50.0	60	4	AAF29121	Aat29121 Oligonuc	c 194	13.6	48.6	25	6	ABN03108
50.0	60	6	ABN47111	ABN47111 Human spl	c 195	13.6	48.6	25	6	ABN03111
50.0	60	6	ABN36352	ABN36352 Human spl	c 196	13.6	48.6	25	6	ABN03110
50.0	60	6	ABN34936	ABN34936 Human spl	c 197	13.6	48.6	25	8	ACK08595
50.0	60	6	ABN39579	ABN39579 Human spl	c 198	13.6	48.6	25	8	ACI08923
49.3	17	7	ACD50464	ACD50464 HBV hamme	c 199	13.6	48.6	25	8	ACI86360
49.3	20	4	AAAS45673	AAAS45673 Human PAR	c 200	13.6	48.6	25	8	ACI55819
49.3	21	2	AAV31343	AAV31343 Phosphati	c 201	13.6	48.6	25	8	ACI43265
49.3	21	2	AAAX15935	AAx15935 PCR prime	c 202	13.6	48.6	27	9	ADE47816
49.3	21	3	AAZ32885	Aaz32885 Human PI	c 203	13.6	48.6	28	2	AAAT90109
49.3	27	2	AAZ27093	Aaz27093 Saccharom	c 204	13.6	48.6	30	6	ABX69917
49.3	29	2	AAV22304	Aav22304 Phosphoro	c 205	13.6	48.6	31	2	AAAT98805
49.3	30	6	ABX68692	ABX68692 Novet Hel	c 206	13.6	48.6	34	2	AAAT85573
49.3	32	2	AAAX06626	AAx06626 Brassica	c 207	13.6	48.6	36	9	ADC02784
49.3	34	3	AAZ51127	Aaz51127 B. napus	c 208	13.6	48.6	36	9	ADC24169
49.3	34	3	AAAS6914	AAAS6914 Human col	c 209	13.6	48.6	39	9	ADC24170
49.3	34	6	ABT12336	ABT12336 Orestes s	c 210	13.6	48.6	39	9	ADC24169
49.3	34	7	ACD91630	ACD91630 Human col	c 211	13.6	48.6	41	8	ACC42053
49.3	35	2	AAAX79948	AAx79948 PCR prime	c 212	13.6	48.6	42	3	AAAO5624
49.3	35	2	AAAX03369	AAx03369 Reverse P	c 213	13.6	48.6	43	3	AAAO5624
49.3	41	2	AAAS6925	AAAS6925 Human col	c 214	13.6	48.6	43	9	ADC24948
49.3	46	6	ABT12347	ABT12347 Orestes s	c 215	13.6	48.6	44	2	AAAT97219
49.3	46	7	ACD91641	ACD91641 Human col	c 216	13.6	48.6	45	8	ADA73846
49.3	50	2	AAQ06722	AAQ06722 HBV LLa2	c 217	13.6	48.6	45	8	ADA73846
49.3	50	4	AAAL33875	AAAL33875 Human SNP	c 218	13.6	48.6	45	8	ADA02300
49.3	50	4	AAAL28618	AAAL28618 Human SNP	c 219	13.6	48.6	45	9	ADB72039
49.3	50	4	AAH79788	Aah79788 Human DNA	c 220	13.6	48.6	47	3	AAZ67025
49.3	50	6	ABZ04325	ABZ04325 Human leu	c 221	13.6	48.6	50	2	AAZ22938
49.3	50	6	ABZ07047	ABZ07047 Human leu	c 222	13.6	48.6	51	5	ABL00814
49.3	50	6	ABZ06231	ABZ06231 Human leu	c 223	13.6	48.6	54	3	AAAG0434
49.3	50	6	ABZ06657	ABZ06657 Human leu	c 224	13.6	48.6	57	2	AAZ20589
49.3	51	2	AAV19093	Aav19093 Synthetic	c 225	13.6	48.6	60	6	ABN38383
49.3	51	2	AAV17997	Aav17997 PCR prime	c 226	13.6	48.6	60	6	ABN38598
49.3	51	4	AAAL27306	AAAL27306 Human SNP	c 227	13.6	48.6	60	6	ABN39145
49.3	51	4	AAAL27331	AAAL27331 Human SNP	c 228	13.6	48.6	60	6	ABN33262
49.3	52	2	AAQ86204	AAQ86204 Sindbis/H	c 229	13.6	48.6	60	6	ABN40951
49.3	52	2	AAAT31151	Aat31151 HDV rever	c 230	13.6	48.6	60	6	ABN46279
49.3	52	2	AAAT30817	Aat30817 HDV riboz	c 231	13.4	47.9	17	7	ACD51872
49.3	52	2	AAV42394	Aav42394 Nested PC	c 232	13.4	47.9	17	7	ACD51871
49.3	52	2	AAV42426	Aav42426 Forward P	c 233	13.4	47.9	20	5	AAAF54564
49.3	52	2	AAV60154	Aav60154 Nested PC	c 234	13.4	47.9	24	7	ABZ22957
49.3	52	2	AAV60185	Aav60185 Reverse P	c 235	13.4	47.9	25	2	AAQ46859
49.3	52	2	AAV70746	Aav70746 Reverse P	c 236	13.4	47.9	25	2	AAAT86146
49.3	52	2	AAV70714	Aav70714 Nested pr	c 237	13.4	47.9	25	8	ACI09244
49.3	52	3	AAZ92930	Aaz92930 Hepatitis	c 238	13.4	47.9	26	2	AAAT08624
49.3	52	3	AAZ92970	Aaz92970 Hepatitis	c 239	13.4	47.9	27	2	AAQ40996
49.3	52	3	AAZ92843	Aaz92843 Hepatitis	c 240	13.4	47.9	27	2	AAQ40995
49.3	52	3	AAZ92803	Aaz92803 Hepatitis	c 241	13.4	47.9	27	2	AAV95527
49.3	52	6	AAAL38850	AAAL38850 Alphaviru	c 242	13.4	47.9	27	2	AAZ08985

47.9	29	2	AAV63201	Probe use	c 316	13.2	47.1	41	6	ABZ46534
47.9	29	3	AAZ39065	Human sec	317	13.2	47.1	41	6	ABL96010
47.9	29	6	ABQ92109	Human pol	c 318	13.2	47.1	41	7	ABX93820
47.9	30	6	ABX68755	Novel Hel	319	13.2	47.1	41	7	ABQ80072
47.9	30	7	AAI53509	Serotonin	c 320	13.2	47.1	42	8	ACD28361
47.9	33	2	AAV26169	PRRS ORF7	321	13.2	47.1	42	2	AAQ65561
47.9	34	3	AAV25815	Adenovirus	322	13.2	47.1	42	7	ABQ80064
47.9	37	8	ACF04588	Method of	c 323	13.2	47.1	50	4	AAI32442
47.9	40	3	AAZ96136	Polynucle	324	13.2	47.1	50	4	AAI32442
47.9	41	6	ABV99601	Human thy	325	13.2	47.1	50	6	ABZ05625
47.9	41	6	ABF88885	Aldehyde/	c 326	13.2	47.1	50	6	ABZ05625
47.9	41	6	ABZ45282	Human car	c 327	13.2	47.1	50	6	ABZ03963
47.9	41	6	ABZ50541	Human car	c 328	13.2	47.1	51	2	AAQ88136
47.9	42	4	AAZ82221	Human ret	329	13.2	47.1	51	3	AAA77076
47.9	43	3	AAZ46872	NF2 gene	330	13.2	47.1	51	4	AAZ85163
47.9	50	4	AAI31813	Human SNP	c 331	13.2	47.1	51	4	AAI27154
47.9	51	3	AAZ77035	Human clo	c 332	13.2	47.1	51	4	AAI33331
47.9	51	4	AAI27304	Human SNP	c 333	13.2	47.1	51	4	AAI27750
47.9	51	4	AAH37768	Human SNP	c 334	13.2	47.1	51	4	AAI27155
47.9	55	3	AAZ35102	Herpesvir	c 335	13.2	47.1	51	4	AAI27156
47.9	55	3	AAZ64355	VAIY1-3F	c 336	13.2	47.1	51	4	AAI27152
47.9	59	7	ABZ57806	Human Igg	337	13.2	47.1	51	4	AAI74313
47.9	60	6	ABK15022	Canine di	c 338	13.2	47.1	54	3	AAZ61059
47.9	60	6	ABK15021	Canine di	339	13.2	47.1	55	7	ABZ53531
47.9	60	6	ABN39741	Human spl	c 340	13.2	47.1	57	3	AAZ44649
47.9	60	6	ABN34224	Human spl	c 341	13.2	47.1	57	6	AAZ43167
47.9	60	6	ABN34336	Human spl	c 342	13.2	47.1	57	7	AAV77288
47.9	60	6	ABN47950	Human spl	343	13.2	47.1	58	7	AAZ48218
47.9	60	6	ABN39303	Human spl	344	13.2	47.1	60	2	AAQ80235
47.1	20	2	AAZ97370	Primer us	c 345	13.2	47.1	60	6	ABN34571
47.1	20	7	ABZ82753	Human HSL	c 346	13.2	47.1	60	6	ABN38627
47.1	21	3	AAI12880	DNA encod	347	13.2	47.1	60	6	ABN39515
47.1	21	4	AAZ97533	Human gen	348	13.2	47.1	60	6	ABN46563
47.1	21	8	ACD67231	PGF carbo	349	13.2	47.1	60	6	ABN41074
47.1	21	9	ADC34630	DNA encod	350	13.2	47.1	60	6	ABN32323
47.1	24	4	AAH00942	Enterobac	c 351	13.2	47.1	60	6	ABN32396
47.1	25	2	AAV58434	PCR prime	c 352	13.2	47.1	60	6	ABN46022
47.1	25	3	AAZ68804	Bacteriop	353	13.2	47.1	60	6	ABN36170
47.1	25	8	ACI19519	Human mic	c 354	13.2	47.1	60	6	ABN36545
47.1	25	8	ACH54522	DNA target	c 355	13.2	47.1	60	6	ABN39928
47.1	26	6	ABK66804	Human gen	c 356	13.2	47.1	60	6	ABN41528
47.1	26	9	ADD01425	Mouse TCH	c 357	13.2	47.1	60	6	ABN45071
47.1	29	3	AAA03821	Polymorph	c 358	13.2	47.1	60	6	ABN43569
47.1	29	7	ABZ68983	PCR prime	c 359	13.2	47.1	60	7	AAZ48215
47.1	30	2	AAQ44285	Sequence	c 360	13	46.4	19	6	ABK85765
47.1	30	4	AAZ95206	Otoferlin	c 361	13	46.4	20	8	ABZ46555
47.1	30	6	ABX70080	Novel Hel	362	13	46.4	20	8	ADA20881
47.1	30	6	ABX68736	Novel Hel	363	13	46.4	20	8	ADA20882
47.1	30	6	ABX67732	Novel Hel	364	13	46.4	20	8	ADA20880
47.1	30	6	ABX37949	RT-PCR pr	365	13	46.4	20	8	ADA20938
47.1	31	7	AAI29642	Human sin	366	13	46.4	21	2	AAZ07376
47.1	31	7	ACD43996	Human gen	367	13	46.4	21	2	AAZ07376
47.1	34	2	AAZ75151	Human ATP	368	13	46.4	21	6	AAV05063
47.1	34	6	AAI47826	Mammalian	369	13	46.4	21	6	ABK33882
47.1	34	8	ACD27624	Human ATP	c 370	13	46.4	21	6	ABL99985
47.1	36	3	AAZ57503	pBR322 Te	371	13	46.4	23	2	AAQ41756
47.1	36	3	AAZ66562	Rat Pas r	c 372	13	46.4	23	2	AAV41068
47.1	36	4	AAI14287	Oligonucle	c 373	13	46.4	24	6	ABK66507
47.1	36	5	ABT97679	Endogenou	374	13	46.4	24	6	ABT88140
47.1	36	6	ABK33266	DNA encod	c 375	13	46.4	24	6	ABT88141
47.1	36	7	AAZ50565	Human CEA	c 376	13	46.4	25	5	AAH28141
47.1	37	2	AAQ80928	Primer fo	c 377	13	46.4	25	7	AAZ55668
47.1	37	9	ADD36388	Human THA	378	13	46.4	25	8	ACI49629
47.1	39	9	ADC42524	FANCD2 PC	c 379	13	46.4	25	8	ACI65229
47.1	41	2	AAQ67351	VCAM 2D-I	380	13	46.4	25	8	ACH60504
47.1	41	2	AAV50540	Brassica	381	13	46.4	26	6	ABT76869
47.1	41	2	AAI15098	PCR prime	382	13	46.4	26	6	ABZ11542
47.1	41	4	AAH73973	Human red	c 383	13	46.4	26	6	ABT11787
47.1	41	4	AAH73972	Human red	c 384	13	46.4	27	2	AAZ08546
47.1	41	6	ABT99980	Human dea	c 385	13	46.4	27	2	AAV12053
47.1	41	6	ABT99979	Human dea	c 386	13	46.4	27	2	AAH21754
47.1	41	6	ABZ49064	Human ALD	c 387	13	46.4	28	3	AAZ27496
47.1	41	6	ABZ49064	Human ALD	388	13	46.4	29	3	AAZ04323

46.4	29	6	ABN85372	Abn85372 Spumaretr	462	12.8	45.7	25	3	AAx82992	AAx82992
46.4	29	9	ADD22842	Add22842 Filamento	463	12.8	45.7	25	4	AAH21680	AAH21680
46.4	30	2	Aaz07825	Aaz07825 Oligo HRP	464	12.8	45.7	25	4	AAH21688	AAH21688
46.4	31	7	ACD43774	Acd43774 Human HRP	465	12.8	45.7	25	4	AH37767	AH37767
46.4	32	8	ABZ81516	Abz81516 Human gen	466	12.8	45.7	25	4	AD10619	AD10619
46.4	33	3	AAA61420	Aaa61420 Human gly	467	12.8	45.7	25	6	ABV85910	ABV85910
46.4	35	7	AD48346	Ad48346 S. cerevi	468	12.8	45.7	25	6	ABV85911	ABV85911
46.4	40	2	AAQ55601	Aaq55601 Flanking	C 469	12.8	45.7	25	6	ABV91561	ABV91561
46.4	41	2	AAV47778	Aav47778 Maize pol	C 470	12.8	45.7	25	6	ABV91560	ABV91560
46.4	41	2	AAV47777	Aav47777 Maize pol	471	12.8	45.7	25	7	AD02934	AD02934
46.4	41	6	ABZ47636	Abz47636 Human ATP	472	12.8	45.7	25	7	AD02935	AD02935
46.4	41	6	ABZ45513	Abz45513 Human ATP	473	12.8	45.7	25	8	ACK09539	ACK09539
46.4	41	6	ABZ45041	Abz45041 Human ATP	C 474	12.8	45.7	25	8	ACI90732	ACI90732
46.4	41	6	ABZ43334	Abz43334 Human N-m	C 475	12.8	45.7	26	3	AA93717	AA93717
46.4	41	6	ABZ48674	Abz48674 Human N-m	C 476	12.8	45.7	26	6	ABK67133	ABK67133
46.4	41	6	ABZ46919	Abz46919 Human ATP	C 477	12.8	45.7	26	6	ABK12970	ABK12970
46.4	41	9	AAU55682	Aal55682 Human Na/	C 478	12.8	45.7	27	2	AA63179	AA63179
46.4	42	2	AAV10835	Aav10835 Human MSH	C 479	12.8	45.7	27	2	AAV98130	AAV98130
46.4	42	6	ABL01835	AbL01835 RNSH2 pre	480	12.8	45.7	29	2	AAQ44286	AAQ44286
46.4	44	7	ABQ80068	Abq80068 T. mariti	481	12.8	45.7	29	2	AAT42344	AAT42344
46.4	45	2	AAQ66712	Aaq66712 Primer to	C 482	12.8	45.7	29	4	AAC97091	AAC97091
46.4	47	3	AAZ65736	Aaz65736 Human map	C 483	12.8	45.7	29	4	AC97164	AC97164
46.4	48	8	AAI62163	Aal62163 Human IL-	C 484	12.8	45.7	29	7	ABT15536	ABT15536
46.4	49	3	AAZ46980	Aaz46980 Human MLH	C 485	12.8	45.7	30	2	AAQ52012	AAQ52012
46.4	50	6	ABZ06157	Abz06157 Human leu	486	12.8	45.7	30	2	AAQ73658	AAQ73658
46.4	50	6	ABZ02986	Abz02986 Human leu	487	12.8	45.7	30	2	AAT33576	AAT33576
46.4	50	6	ABZ07651	Abz07651 Human leu	488	12.8	45.7	30	2	AAT29635	AAT29635
46.4	51	4	AAI32903	Aal32903 Human SNP	C 490	12.8	45.7	30	2	AAV75149	AAV75149
46.4	51	4	AAI75897	Aai75897 Human sll	C 491	12.8	45.7	30	2	AAV64108	AAV64108
46.4	51	4	AAH90525	Aah90525 Human cto	C 492	12.8	45.7	30	6	ABX69054	ABX69054
46.4	54	3	AAZ73942	Aaz73942 GFP ile/A	493	12.8	45.7	30	8	ABA93865	ABA93865
46.4	58	3	AAZ29736	Aaz29736 Primer-2	C 494	12.8	45.7	30	8	ACD27622	ACD27622
46.4	58	7	ACA89879	Aca89879 Human IL-	C 495	12.8	45.7	31	3	AA78753	AA78753
46.4	58	7	ACA89879	Aca89879 Human IL-	C 496	12.8	45.7	32	6	AAI17090	AAI17090
46.4	58	7	ACA84663	Aca84663 Human int	C 497	12.8	45.7	32	6	AAI20633	AAI20633
46.4	58	8	ADA43262	Ada43262 Human int	C 498	12.8	45.7	32	6	ABA00367	ABA00367
46.4	58	8	ADA49803	Ada49803 Human int	499	12.8	45.7	33	4	AAQ69053	AAQ69053
46.4	58	9	AD66997	Ad66997 Human IL-	C 500	12.8	45.7	33	5	AAH48364	AAH48364
46.4	58	9	AD66997	Ad66997 Human IL-	C 501	12.8	45.7	33	6	ABQ77965	ABQ77965
46.4	60	6	ABN47374	Abn47374 Human spl	C 502	12.8	45.7	33	6	AAI53835	AAI53835
46.4	60	6	ABN44408	Abn44408 Human spl	C 503	12.8	45.7	33	6	ABK49118	ABK49118
46.4	60	6	ABN42474	Abn42474 Human spl	C 504	12.8	45.7	33	7	ACF06227	ACF06227
46.4	60	6	ABN35722	Abn35722 Human spl	C 505	12.8	45.7	36	2	AAQ77835	AAQ77835
46.4	60	6	ABN45654	Abn45654 Human spl	C 506	12.8	45.7	36	4	AAQ02111	AAQ02111
46.4	60	6	ABN40427	Abn40427 Human spl	C 507	12.8	45.7	36	4	AAH50206	AAH50206
46.4	60	6	ABN42615	Abn42615 Human spl	C 508	12.8	45.7	36	7	ACD26342	ACD26342
46.4	60	6	ABN32591	Abn32591 Human spl	C 509	12.8	45.7	37	3	AAZ38564	AAZ38564
46.4	60	6	ABN44580	Abn44580 Human spl	510	12.8	45.7	38	2	AAV63951	AAV63951
46.4	60	6	ABN35306	Abn35306 Human spl	511	12.8	45.7	38	2	AAH81030	AAH81030
46.4	60	6	ABN45676	Abn45676 Human spl	C 512	12.8	45.7	38	8	ACC99668	ACC99668
46.4	60	6	ABN46934	Abn46934 Human spl	C 513	12.8	45.7	38	8	ACC99674	ACC99674
46.4	60	6	ABN42631	Abn42631 HLA Class	C 514	12.8	45.7	41	7	ABZ25886	ABZ25886
46.4	60	6	ABN42631	Abn42631 HLA Class	C 515	12.8	45.7	41	7	ABZ25886	ABZ25886
46.4	60	6	ABN42631	Abn42631 HLA Class	C 516	12.8	45.7	41	7	ABZ25886	ABZ25886
46.4	60	6	ABN42631	Abn42631 HLA Class	C 517	12.8	45.7	42	2	AAQ75448	AAQ75448
46.4	60	6	ABN42631	Abn42631 HLA Class	C 518	12.8	45.7	42	6	ABK13824	ABK13824
46.4	60	6	ABN42631	Abn42631 HLA Class	519	12.8	45.7	43	2	AAQ53774	AAQ53774
46.4	60	6	ABN42631	Abn42631 HLA Class	C 520	12.8	45.7	43	2	AAQ75450	AAQ75450
46.4	60	6	ABN42631	Abn42631 HLA Class	521	12.8	45.7	43	2	AAT07975	AAT07975
46.4	60	6	ABN42631	Abn42631 HLA Class	522	12.8	45.7	43	2	AAV00991	AAV00991
46.4	60	6	ABN42631	Abn42631 HLA Class	523	12.8	45.7	43	2	AAV14776	AAV14776
46.4	60	6	ABN42631	Abn42631 HLA Class	524	12.8	45.7	43	2	AAV79851	AAV79851
46.4	60	6	ABN42631	Abn42631 HLA Class	525	12.8	45.7	43	3	AAA92951	AAA92951
46.4	60	6	ABN42631	Abn42631 HLA Class	526	12.8	45.7	43	6	ABK61327	ABK61327
46.4	60	6	ABN42631	Abn42631 HLA Class	527	12.8	45.7	43	6	AAH80088	AAH80088
46.4	60	6	ABN42631	Abn42631 HLA Class	528	12.8	45.7	45	3	AAI58514	AAI58514
46.4	60	6	ABN42631	Abn42631 HLA Class	529	12.8	45.7	45	3	AAQ01258	AAQ01258
46.4	60	6	ABN42631	Abn42631 HLA Class	530	12.8	45.7	45	3	AAA49494	AAA49494
46.4	60	6	ABN42631	Abn42631 HLA Class	531	12.8	45.7	45	3	AAA46913	AAA46913
46.4	60	6	ABN42631	Abn42631 HLA Class	532	12.8	45.7	45	5	AAH26512	AAH26512
46.4	60	6	ABN42631	Abn42631 HLA Class	C 533	12.8	45.7	45	7	ABX75476	ABX75476
46.4	60	6	ABN42631	Abn42631 HLA Class	534	12.8	45.7	45	7	ABX89467	ABX89467

45.7	45	7	ABX96804	Abx96804 Human PRO	608	12.6	45.0	25	2	AAV08069	AAV08069
45.7	45	7	ABX78458	Abx78458 Novel hum	c 609	12.6	45.0	25	2	AAV08070	AAV08070
45.7	45	7	ABX77092	Abx77092 Human PRO	c 610	12.6	45.0	25	2	AAV08071	AAV08071
45.7	45	7	ABX75923	Abx75923 Human PRO	c 611	12.6	45.0	25	2	AAV08072	AAV08072
45.7	45	7	ABX89634	Abx89634 Novel hum	c 612	12.6	45.0	25	2	AAV08073	AAV08073
45.7	45	7	ABX34120	Abx34120 Human pro	c 613	12.6	45.0	25	2	AAV08074	AAV08074
45.7	45	8	ACA04340	ACA04340 Human PRO	c 614	12.6	45.0	25	2	AAV08075	AAV08075
45.7	45	9	ADC25804	ADC25804 Human sec	c 615	12.6	45.0	25	2	AAV08076	AAV08076
45.7	45	9	ADC25562	ADC25562 Human sec	c 616	12.6	45.0	25	2	AAV08077	AAV08077
45.7	45	10	ADP711517	ADP711517 Human sec	c 617	12.6	45.0	25	2	AAV08078	AAV08078
45.7	45	8	ACF06072	ACF06072 Immunoco	c 618	12.6	45.0	25	2	AAV08079	AAV08079
45.7	45	3	AAZ62249	AAZ62249 PCR prime	c 619	12.6	45.0	25	2	AAV08080	AAV08080
45.7	45	3	AAZ67039	AAZ67039 Human map	c 620	12.6	45.0	25	2	AAV08081	AAV08081
45.7	45	3	AAZ67834	AAZ67834 Human map	c 621	12.6	45.0	25	2	AAV08082	AAV08082
45.7	45	9	ADC20023	ADC20023 Synthetic	c 622	12.6	45.0	25	2	AAV08083	AAV08083
45.7	45	2	AAZ36834	AAZ36834 Primer P2	c 623	12.6	45.0	25	2	AAV08084	AAV08084
45.7	45	6	ABQ82468	ABQ82468 Glo gene	c 624	12.6	45.0	25	2	AAV08085	AAV08085
45.7	45	4	AAZ29184	AAZ29184 Human SNP	c 625	12.6	45.0	25	2	AAV08086	AAV08086
45.7	45	4	AAZ29185	AAZ29185 Human SNP	c 626	12.6	45.0	25	2	AAV08087	AAV08087
45.7	45	6	ABZ02766	ABZ02766 Human leu	c 627	12.6	45.0	25	2	AAV08088	AAV08088
45.7	45	51	AAQ86173	AAQ86173 Primer HD	c 628	12.6	45.0	25	2	AAV08089	AAV08089
45.7	45	3	AAZ57513	AAZ57513 Kunitz pr	c 629	12.6	45.0	25	2	AAV08090	AAV08090
45.7	45	4	AAZ127635	AAZ127635 Human SNP	c 630	12.6	45.0	25	2	AAV08091	AAV08091
45.7	45	4	AAZ174798	AAZ174798 Human sil	c 631	12.6	45.0	25	2	AAV08092	AAV08092
45.7	45	4	AAZ174799	AAZ174799 Human sil	c 632	12.6	45.0	25	2	AAV08093	AAV08093
45.7	45	4	AAZ178394	AAZ178394 Human sil	c 633	12.6	45.0	25	2	AAV08094	AAV08094
45.7	45	4	AAZ178394	AAZ178394 Human sil	c 634	12.6	45.0	25	2	AAV08095	AAV08095
45.7	45	4	AAZ14293	AAZ14293 Human DNA	c 635	12.6	45.0	25	2	AAV08096	AAV08096
45.7	45	6	ABQ82469	ABQ82469 Mito gene	c 636	12.6	45.0	25	2	AAV08097	AAV08097
45.7	45	6	ABN86455	ABN86455 M. tuberc	c 637	12.6	45.0	25	2	AAV08098	AAV08098
45.7	45	2	AAV90106	AAV90106 Ha-ras fr	c 638	12.6	45.0	25	2	AAV08099	AAV08099
45.7	45	2	AAV40200	AAV40200 Escherich	c 639	12.6	45.0	25	2	AAV08100	AAV08100
45.7	45	60	AAZ59927	AAZ59927 Canine Ig	c 640	12.6	45.0	25	2	AAV08101	AAV08101
45.7	45	60	AAZ59928	AAZ59928 Canine Ig	c 641	12.6	45.0	25	2	AAV08102	AAV08102
45.7	45	60	ABN42793	ABN42793 Human sil	c 642	12.6	45.0	25	2	AAV08103	AAV08103
45.7	45	60	ABN45626	ABN45626 Human sil	c 643	12.6	45.0	25	2	AAV08104	AAV08104
45.7	45	60	ABN37545	ABN37545 Human spl	c 644	12.6	45.0	25	2	AAV08105	AAV08105
45.7	45	60	ABN41628	ABN41628 Human spl	c 645	12.6	45.0	25	2	AAV08106	AAV08106
45.7	45	60	ABN46450	ABN46450 Human spl	c 646	12.6	45.0	25	2	AAV08107	AAV08107
45.7	45	60	ABN42218	ABN42218 Human spl	c 647	12.6	45.0	25	2	AAV08108	AAV08108
45.7	45	60	ABN46438	ABN46438 Human spl	c 648	12.6	45.0	25	2	AAV08109	AAV08109
45.7	45	60	ABN33226	ABN33226 Human spl	c 649	12.6	45.0	25	2	AAV08110	AAV08110
45.7	45	60	ABN41292	ABN41292 Human spl	c 650	12.6	45.0	25	2	AAV08111	AAV08111
45.7	45	60	ABN36922	ABN36922 Human spl	c 651	12.6	45.0	25	2	AAV08112	AAV08112
45.7	45	60	ABN37802	ABN37802 Human spl	c 652	12.6	45.0	25	2	AAV08113	AAV08113
45.7	45	60	ABT13055	ABT13055 Human apo	c 653	12.6	45.0	25	2	AAV08114	AAV08114
45.7	45	19	ABZ66622	ABZ66622 Loop 3-4	c 654	12.6	45.0	25	2	AAV08115	AAV08115
45.7	45	20	AAZ13463	AAZ13463 B. thurin	c 655	12.6	45.0	25	2	AAV08116	AAV08116
45.7	45	20	AAZ04955	AAZ04955 PCR prime	c 656	12.6	45.0	25	2	AAV08117	AAV08117
45.7	45	20	AAZ58910	AAZ58910 Cry3A pri	c 657	12.6	45.0	25	2	AAV08118	AAV08118
45.7	45	20	AAZ166887	AAZ166887 Nucleotid	c 658	12.6	45.0	25	2	AAV08119	AAV08119
45.7	45	20	AAZ19679	AAZ19679 Heat choc	c 659	12.6	45.0	25	2	AAV08120	AAV08120
45.7	45	20	ABK49845	ABK49845 Mouse ADA	c 660	12.6	45.0	25	2	AAV08121	AAV08121
45.7	45	20	ABZ25628	ABZ25628 Human con	c 661	12.6	45.0	25	2	AAV08122	AAV08122
45.7	45	21	AAZ73452	AAZ73452 SNP flank	c 662	12.6	45.0	25	2	AAV08123	AAV08123
45.7	45	21	AAZ69914	AAZ69914 Oligonuc	c 663	12.6	45.0	25	2	AAV08124	AAV08124
45.7	45	21	AAZ69578	AAZ69578 Human gen	c 664	12.6	45.0	25	2	AAV08125	AAV08125
45.7	45	21	ABZ60270	ABZ60270 Human pol	c 665	12.6	45.0	25	2	AAV08126	AAV08126
45.7	45	21	ABZ60269	ABZ60269 Human pol	c 666	12.6	45.0	25	2	AAV08127	AAV08127
45.7	45	21	ABZ60268	ABZ60268 Human pol	c 667	12.6	45.0	25	2	AAV08128	AAV08128
45.7	45	21	ABZ60267	ABZ60267 Human pol	c 668	12.6	45.0	25	2	AAV08129	AAV08129
45.7	45	21	ABZ60266	ABZ60266 Human pol	c 669	12.6	45.0	25	2	AAV08130	AAV08130
45.7	45	21	ABZ60265	ABZ60265 Human met	c 670	12.6	45.0	25	2	AAV08131	AAV08131
45.7	45	22	AAZ09690	AAZ09690 Human met	c 671	12.6	45.0	25	2	AAV08132	AAV08132
45.7	45	22	AAZ50636	AAZ50636 Methylene	c 672	12.6	45.0	25	2	AAV08133	AAV08133
45.7	45	22	AAZ20464	AAZ20464 Human MTH	c 673	12.6	45.0	25	2	AAV08134	AAV08134
45.7	45	22	ABK13525	ABK13525 Methylene	c 674	12.6	45.0	25	2	AAV08135	AAV08135
45.7	45	22	ABN89155	ABN89155 Human GPC	c 675	12.6	45.0	25	2	AAV08136	AAV08136
45.7	45	22	ABT04595	ABT04595 Human NMO	c 676	12.6	45.0	25	2	AAV08137	AAV08137
45.7	45	22	ABZ59399	ABZ59399 Human pro	c 677	12.6	45.0	25	2	AAV08138	AAV08138
45.7	45	24	AAV17123	AAV17123 Metabolo	c 678	12.6	45.0	25	2	AAV08139	AAV08139
45.7	45	24	ABQ77730	ABQ77730 Cypress p	c 679	12.6	45.0	25	2	AAV08140	AAV08140
45.7	45	24	ACC48183	ACC48183 Angiotens	c 680	12.6	45.0	25	2	AAV08141	AAV08141

43	45.0	43	AAC82225	Aac82225 Human ret	754	12.6	45.0	60	7	ABZ58855
44	45.0	44	AAQ83198	Aaq83198 Synthetic	755	12.4	44.3	15	7	ACD56646
45	45.0	45	AAQ83198	Aaq83198 Synthetic	c 756	12.4	44.3	17	7	ABT36991
46	45.0	46	AAQ83198	Aaq83198 Synthetic	757	12.4	44.3	17	7	ACD50465
47	45.0	47	AAQ83198	Aaq83198 Synthetic	c 758	12.4	44.3	17	9	ABD40878
48	45.0	48	AAQ83198	Aaq83198 Synthetic	c 759	12.4	44.3	20	2	AAZ21239
49	45.0	49	AAQ83198	Aaq83198 Synthetic	c 760	12.4	44.3	22	2	AAV63757
50	45.0	50	AAQ83198	Aaq83198 Synthetic	c 761	12.4	44.3	22	2	AAV63757
51	45.0	51	AAQ83198	Aaq83198 Synthetic	c 762	12.4	44.3	23	6	ABL40521
52	45.0	52	AAQ83198	Aaq83198 Synthetic	763	12.4	44.3	23	7	ABZ57958
53	45.0	53	AAQ83198	Aaq83198 Synthetic	c 764	12.4	44.3	24	2	AAV68426
54	45.0	54	AAQ83198	Aaq83198 Synthetic	c 765	12.4	44.3	24	5	AAQ80803
55	45.0	55	AAQ83198	Aaq83198 Synthetic	c 766	12.4	44.3	24	6	AAQ30498
56	45.0	56	AAQ83198	Aaq83198 Synthetic	c 767	12.4	44.3	24	6	AAQ49849
57	45.0	57	AAQ83198	Aaq83198 Synthetic	c 768	12.4	44.3	25	4	AAQ14659
58	45.0	58	AAQ83198	Aaq83198 Synthetic	c 769	12.4	44.3	25	6	ABV91558
59	45.0	59	AAQ83198	Aaq83198 Synthetic	c 770	12.4	44.3	25	6	ABV91559
60	45.0	60	AAQ83198	Aaq83198 Synthetic	771	12.4	44.3	25	6	ABK67703
61	45.0	61	AAQ83198	Aaq83198 Synthetic	c 772	12.4	44.3	25	8	ACI56469
62	45.0	62	AAQ83198	Aaq83198 Synthetic	c 773	12.4	44.3	25	8	ACI60966
63	45.0	63	AAQ83198	Aaq83198 Synthetic	c 774	12.4	44.3	25	8	ACI43217
64	45.0	64	AAQ83198	Aaq83198 Synthetic	c 775	12.4	44.3	25	8	ACI34002
65	45.0	65	AAQ83198	Aaq83198 Synthetic	776	12.4	44.3	25	8	ACI53000
66	45.0	66	AAQ83198	Aaq83198 Synthetic	c 777	12.4	44.3	25	8	ACI96152
67	45.0	67	AAQ83198	Aaq83198 Synthetic	c 778	12.4	44.3	25	8	ACI55841
68	45.0	68	AAQ83198	Aaq83198 Synthetic	c 779	12.4	44.3	25	8	ACI43216
69	45.0	69	AAQ83198	Aaq83198 Synthetic	c 780	12.4	44.3	25	9	ADB88629
70	45.0	70	AAQ83198	Aaq83198 Synthetic	c 781	12.4	44.3	26	5	AAH11253
71	45.0	71	AAQ83198	Aaq83198 Synthetic	782	12.4	44.3	26	6	ABK90386
72	45.0	72	AAQ83198	Aaq83198 Synthetic	783	12.4	44.3	27	2	AAH89091
73	45.0	73	AAQ83198	Aaq83198 Synthetic	784	12.4	44.3	27	5	AAH25501
74	45.0	74	AAQ83198	Aaq83198 Synthetic	785	12.4	44.3	27	5	AAH25501
75	45.0	75	AAQ83198	Aaq83198 Synthetic	786	12.4	44.3	27	8	AAH50124
76	45.0	76	AAQ83198	Aaq83198 Synthetic	787	12.4	44.3	27	8	ACD27779
77	45.0	77	AAQ83198	Aaq83198 Synthetic	788	12.4	44.3	29	2	AAQ67090
78	45.0	78	AAQ83198	Aaq83198 Synthetic	789	12.4	44.3	29	2	AAQ67211
79	45.0	79	AAQ83198	Aaq83198 Synthetic	c 790	12.4	44.3	29	2	AAH89093
80	45.0	80	AAQ83198	Aaq83198 Synthetic	c 791	12.4	44.3	29	3	AAH04171
81	45.0	81	AAQ83198	Aaq83198 Synthetic	792	12.4	44.3	29	5	AAH25503
82	45.0	82	AAQ83198	Aaq83198 Synthetic	793	12.4	44.3	29	7	AAH50126
83	45.0	83	AAQ83198	Aaq83198 Synthetic	794	12.4	44.3	29	8	ACD27781
84	45.0	84	AAQ83198	Aaq83198 Synthetic	795	12.4	44.3	29	8	ACD40541
85	45.0	85	AAQ83198	Aaq83198 Synthetic	796	12.4	44.3	30	2	AAH89094
86	45.0	86	AAQ83198	Aaq83198 Synthetic	c 797	12.4	44.3	30	2	AAH89094
87	45.0	87	AAQ83198	Aaq83198 Synthetic	c 798	12.4	44.3	30	5	ABT36991
88	45.0	88	AAQ83198	Aaq83198 Synthetic	799	12.4	44.3	30	5	ABT36991
89	45.0	89	AAQ83198	Aaq83198 Synthetic	c 800	12.4	44.3	30	6	ABX68134
90	45.0	90	AAQ83198	Aaq83198 Synthetic	801	12.4	44.3	30	6	ABX68745
91	45.0	91	AAQ83198	Aaq83198 Synthetic	802	12.4	44.3	30	6	ABX68723
92	45.0	92	AAQ83198	Aaq83198 Synthetic	803	12.4	44.3	30	6	ABX69509
93	45.0	93	AAQ83198	Aaq83198 Synthetic	804	12.4	44.3	30	6	ABX69519
94	45.0	94	AAQ83198	Aaq83198 Synthetic	805	12.4	44.3	30	6	AAH27904
95	45.0	95	AAQ83198	Aaq83198 Synthetic	806	12.4	44.3	30	7	AAH50127
96	45.0	96	AAQ83198	Aaq83198 Synthetic	807	12.4	44.3	30	8	ACD27782
97	45.0	97	AAQ83198	Aaq83198 Synthetic	808	12.4	44.3	30	8	ACD40542
98	45.0	98	AAQ83198	Aaq83198 Synthetic	c 809	12.4	44.3	30	9	ADD67377
99	45.0	99	AAQ83198	Aaq83198 Synthetic	c 810	12.4	44.3	31	2	AAZ22146
100	45.0	100	AAQ83198	Aaq83198 Synthetic	811	12.4	44.3	31	2	AAH89095
101	45.0	101	AAQ83198	Aaq83198 Synthetic	812	12.4	44.3	31	5	AAH25505
102	45.0	102	AAQ83198	Aaq83198 Synthetic	813	12.4	44.3	31	6	ABK66150
103	45.0	103	AAQ83198	Aaq83198 Synthetic	814	12.4	44.3	31	7	ABK66150
104	45.0	104	AAQ83198	Aaq83198 Synthetic	c 815	12.4	44.3	31	8	ACF05531
105	45.0	105	AAQ83198	Aaq83198 Synthetic	816	12.4	44.3	31	8	ACF05530
106	45.0	106	AAQ83198	Aaq83198 Synthetic	817	12.4	44.3	31	8	ACD27783
107	45.0	107	AAQ83198	Aaq83198 Synthetic	818	12.4	44.3	31	8	ACD40543
108	45.0	108	AAQ83198	Aaq83198 Synthetic	c 819	12.4	44.3	32	2	AAQ93346
109	45.0	109	AAQ83198	Aaq83198 Synthetic	c 820	12.4	44.3	32	2	AAQ93346
110	45.0	110	AAQ83198	Aaq83198 Synthetic	c 821	12.4	44.3	32	2	AAQ93346
111	45.0	111	AAQ83198	Aaq83198 Synthetic	c 822	12.4	44.3	32	2	AAQ93346
112	45.0	112	AAQ83198	Aaq83198 Synthetic	c 823	12.4	44.3	32	2	AAQ93346
113	45.0	113	AAQ83198	Aaq83198 Synthetic	c 824	12.4	44.3	32	2	AAQ93346
114	45.0	114	AAQ83198	Aaq83198 Synthetic	c 825	12.4	44.3	32	2	AAQ93346
115	45.0	115	AAQ83198	Aaq83198 Synthetic	c 826	12.4	44.3	32	2	AAQ93346

44.3	32	2	AAT78674	Rat78674 Primer 5p	900	12.4	44.3	41	6	ABZ47942	Abz47942
44.3	32	2	AAT87102	Aat87102 SELEX PCR	C 901	12.4	44.3	41	6	ABZ45805	Abz45805
44.3	32	2	AAT19550	Aat19550 Complemen	C 902	12.4	44.3	41	6	ABZ46151	Abz46151
44.3	32	2	AAT31104	Aat31104 SELEX PCR	C 903	12.4	44.3	41	6	ABZ50218	Abz50218
44.3	32	3	AAT52789	Aat52789 PCR prime	904	12.4	44.3	41	6	ABZ45595	Abz45595
44.3	32	3	AAZ40148	C. tetani	905	12.4	44.3	41	7	ABX50132	Abx50132
44.3	32	3	AAC69845	Aac69845 SELEX PCR	C 906	12.4	44.3	41	7	ABX75154	Abx75154
44.3	32	4	AAF56864	Aaf56864 4ON7a ssd	907	12.4	44.3	41	8	ACD27787	Acd27787
44.3	32	4	AAF70637	Aaf70637 SELEX exp	908	12.4	44.3	41	8	ACD40547	Acd40547
44.3	32	5	AAF90705	Aaf90705 SELEX PCR	C 909	12.4	44.3	42	2	AAV57974	Aav57974
44.3	32	6	ABL41378	AbL41378 Human G-s	C 910	12.4	44.3	42	2	AAV10877	Aav10877
44.3	32	6	ABL57272	AbL57272 5N7 prime	C 911	12.4	44.3	42	3	AAA07291	Aaa07291
44.3	32	8	ADA21795	Ada21795 HGF 3ON7	912	12.4	44.3	42	4	AAI33783	Aai33783
44.3	33	2	AAT78601	Aat78601 Primer #1	913	12.4	44.3	43	2	AAQ45693	Aaq45693
44.3	33	2	AAH89097	Aah89097 SXR direc	C 914	12.4	44.3	43	2	AAV71144	Aav71144
44.3	33	3	AAH89096	Aah89096 SXR direc	915	12.4	44.3	43	2	AAV32572	Aav32572
44.3	33	5	AAH25506	Aah25506 Steroid-a	916	12.4	44.3	43	2	AAV26870	Aav26870
44.3	33	5	AAH25507	Aah25507 Steroid-a	C 917	12.4	44.3	43	2	AAV27603	Aav27603
44.3	33	6	ABQ38892	Abq38892 Human mac	C 918	12.4	44.3	43	6	AAJ30589	Aaj30589
44.3	33	6	AB199977	Abi99977 Human dea	C 919	12.4	44.3	44	3	AAA98736	Aaa98736
44.3	33	7	AAD50129	Aad50129 SXR respo	C 921	12.4	44.3	44	3	AAQ28462	Aaq28462
44.3	33	8	ACD27784	Acd27784 SXR DNA b	922	12.4	44.3	44	7	AAQ72666	Aaq72666
44.3	33	8	ACD27785	Acd27785 SXR DNA b	923	12.4	44.3	44	7	ABQ80082	Abq80082
44.3	33	8	ACD40544	Acd40544 Direct re	924	12.4	44.3	45	2	AAH58007	Aah58007
44.3	33	8	ACD40545	Acd40545 Direct re	925	12.4	44.3	45	2	AAH51403	Aah51403
44.3	34	3	AAA75581	Aaa75581 PCR prime	C 926	12.4	44.3	46	6	ABQ96530	Abq96530
44.3	34	6	AAH20689	Aah20689 Mouse zal	C 927	12.4	44.3	46	7	ABZ68916	Abz68916
44.3	35	2	AAQ54464	Aaq54464 Mycoplasm	C 928	12.4	44.3	47	6	ABK96282	Abk96282
44.3	35	2	AAQ45183	Aat45183 Mycoplasm	C 929	12.4	44.3	49	9	ABL50615	AbL50615
44.3	35	2	AAT45163	Aat45163 Mycoplasm	C 930	12.4	44.3	50	2	ADQ99551	Adq99551
44.3	35	2	AAV49334	Aav49334 Primer AB	931	12.4	44.3	50	2	AAQ50268	Aaq50268
44.3	36	2	AAH15800	Aah15800 PCR prime	932	12.4	44.3	50	2	AAT74727	Aat74727
44.3	36	2	AAH89098	Aah89098 SXR direc	933	12.4	44.3	50	4	AAH26885	Aah26885
44.3	36	3	AAA28459	Aaa28459 Oligonuc	934	12.4	44.3	50	6	AAH45616	Aah45616
44.3	36	3	AAA46527	Aaa46527 PCR prime	935	12.4	44.3	50	6	ADQ24217	Adq24217
44.3	36	5	AAH25508	Aah25508 Steroid-a	C 936	12.4	44.3	50	7	AAH4793	Aah4793
44.3	36	7	AAH50111	Aad50111 SXR respo	C 937	12.4	44.3	51	2	AAT70196	Aat70196
44.3	36	8	ACD27786	Acd27786 SXR DNA b	C 938	12.4	44.3	51	4	AAI27751	Aai27751
44.3	37	3	AAH70159	Aah70159 T7 promot	C 939	12.4	44.3	51	4	AAI27390	Aai27390
44.3	37	4	AAH25817	Aah25817 Human/mou	C 940	12.4	44.3	51	4	AAI32515	Aai32515
44.3	38	2	AAQ32288	Aaq32288 Barley le	941	12.4	44.3	51	4	AAI32016	Aai32016
44.3	38	4	ABK04754	Abk04754 Human NOG	C 942	12.4	44.3	51	4	AAI33336	Aai33336
44.3	38	7	ACD50514	Acd50514 HBV hamme	C 943	12.4	44.3	51	4	AAI27366	Aai27366
44.3	38	7	ACD52458	Acd52458 HBV inozy	C 944	12.4	44.3	51	4	AAI73852	Aai73852
44.3	39	7	ACF56962	Acf56962 DGI-3 PCR	C 945	12.4	44.3	51	4	AAI75831	Aai75831
44.3	40	2	AAT14232	Aat14232 Primer SP	C 946	12.4	44.3	51	4	AAI79579	Aai79579
44.3	40	2	AAT42817	Aat42817 Primer #3	C 947	12.4	44.3	51	4	AAI73850	Aai73850
44.3	40	2	AAH87104	Aat87104 Primer 5p	C 948	12.4	44.3	51	4	AAI79719	Aai79719
44.3	40	2	AAH85061	Aah85061 PCR prime	949	12.4	44.3	51	4	AAI73853	Aai73853
44.3	40	6	ABT12259	Abt12259 E coli ex	950	12.4	44.3	51	5	AAH79535	Aah79535
44.3	40	6	ABT12254	Abt12254 E coli ex	C 951	12.4	44.3	51	5	AAH79535	Aah79535
44.3	40	6	ABT12214	Abt12214 E coli ex	C 952	12.4	44.3	52	4	AAH79535	Aah79535
44.3	40	7	ACC43714	Acc43714 PCR prime	C 953	12.4	44.3	52	4	AAH79535	Aah79535
44.3	40	7	ADA48879	Aad48879 PCR prime	C 954	12.4	44.3	52	5	AAH79535	Aah79535
44.3	40	7	ABQ80076	Abq80076 T. mariti	C 955	12.4	44.3	52	7	ADA47349	Ada47349
44.3	41	2	AAH35888	Aah35888 Marek Dis	956	12.4	44.3	53	2	AAZ10169	Aaz10169
44.3	41	2	AAT39323	Aat39323 Primer CD	C 957	12.4	44.3	53	6	AAH43267	Aah43267
44.3	41	2	AAT35920	Aat35920 Marek Dis	C 958	12.4	44.3	54	2	AAV60892	Aav60892
44.3	41	2	AAV42533	Aav42533 PCR prime	C 959	12.4	44.3	54	7	ABX94281	Abx94281
44.3	41	2	AAH89099	Aah89099 SXR direc	C 960	12.4	44.3	54	9	ADQ54963	Adq54963
44.3	41	2	AAZ61052	Aaz61052 PCR prime	C 961	12.4	44.3	56	2	AAT74726	Aat74726
44.3	41	3	AAH25509	Aah25509 Steroid-a	962	12.4	44.3	57	3	AAQ63713	Aaq63713
44.3	41	5	AAH48366	Aah48366 Aldehyde-	963	12.4	44.3	57	3	AAI11183	Aai11183
44.3	41	5	ABZ72301	Abz72301 Gene 216	C 964	12.4	44.3	58	2	AAV15196	Aav15196
44.3	41	6	ABK47539	Abk47539 Avidin 9	C 965	12.4	44.3	58	3	AAZ35103	Aaz35103
44.3	41	6	ABK47538	Abk47538 Avidin 9	C 966	12.4	44.3	59	4	AAH26556	Aah26556
44.3	41	6	ABZ70769	Abz70769 Human zin	C 967	12.4	44.3	59	7	ABX94759	Abx94759
44.3	41	6	ABZ45596	Abz45596 Human ATP	968	12.4	44.3	60	2	AAQ75286	Aaq75286
44.3	41	6	ABZ47941	Abz47941 Human ATP	969	12.4	44.3	60	2	AAT27716	Aat27716
44.3	41	6			C 971	12.4	44.3	60	6	AAH36603	Aah36603
44.3	41	6			C 972	12.4	44.3	60	6	ADQ35279	Adq35279
44.3	41	6				12.4	44.3	60	6	ABN45971	Abn45971

44.3 60 6 ABN36828 Human spl
 44.3 60 6 ABN35852 Human spl
 44.3 60 6 ABN38394 Human spl
 44.3 60 6 ABN40449 Human spl
 44.3 60 6 ABN32230 Human spl
 44.3 60 6 ABN58873 Human spl
 44.3 60 6 ABN32787 Human spl
 44.3 60 6 ABN42207 Human spl
 44.3 60 6 ABN36167 Human spl
 44.3 60 6 ABN34404 Human spl
 44.3 60 6 ABN44236 Human spl
 44.3 60 6 ABN39531 Human spl
 44.3 60 6 ABN43076 Human spl
 44.3 60 6 ABN58663 Human spl
 44.3 60 6 ABN35048 Human spl
 44.3 60 6 ABN45323 Human spl
 44.3 60 6 ABN39998 Human spl
 44.3 60 7 ACD07797 Cholesterol
 43.6 17 3 AAF07343 Hammerhead
 43.6 17 7 ABT34426 Tumour su
 43.6 17 7 ACC64892 Murine ol
 43.6 17 9 ADC04115 Human Na/
 43.6 18 4 AAH77481 Mandrill
 43.6 19 6 ABK33800 Human inh
 43.6 19 6 ABS59907 Human DNA
 43.6 20 2 AAQ39568 PCR Prime
 43.6 20 2 AAV26799 Rhodococ
 43.6 20 2 AAX80916 Antisense

ALIGNMENTS

standard; DNA; 28 BP.

2 (first entry)

ontrol probe SEQ ID NO:23.

; carcinoembryonic antigen; adenocarcinoma; oesophagus;
 ; probe; ss.

1-A1.

2.

2; 2002WO-US006504.

1; 2001US-0273277P.

IV PITTSBURGH.

; Luketich JD, Raja S, Kelly LA, Finkelstein SD;

732795/79.

PCR method for detecting malignancies, e.g. adenocarcinoma of
 Gus comprises conducting a PCR amplification on a DNA sample in
 tion mixture.

Page 78; 141pp; English.

it invention describes a multiplex polymerase chain reaction
 comprising conducting PCR on a DNA sample in a reaction
 conducted in first and second amplification stages, each with one
 R cycles comprising denaturing, annealing and elongating steps
 elongating step may be conducted at the same temperature as the

CC annealing step. The second amplification stage of (M1) is condi
 CC different reaction conditions from that of the first amplifica
 CC to modulate the relative rate of production of the first ampli
 CC first primer set and a second amplicon by a second primer set
 CC first and second amplification stages. Also described: (1) an
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) int
 CC PCR diagnostic; (3) rapid detection of a malignancy or of meta
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use i
 CC automated PCR system. (M1) is useful for detecting malignancie
 CC adenocarcinoma of the oesophagus. (M1) eliminates contaminatio
 CC decreases the time it takes to carry out a PCR reaction. The p
 CC sequence represents an internal control probe, which is used i
 CC example from the present invention

XX SQ Sequence 28 BP; 6 A; 8 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 6; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.021; Mismatches 0; Indels 0;

Matches 28; Conservative 0; Mismatches 0; Indels 0;

QY 1 AGCATCATCCTCTGCATGTCAGGTCAAT 28

Db 1 AGCATCATCCTCTGCATGTCAGGTCAAT 28

RESULT 2

AAV84287

ID AAV84287 standard; DNA; 20 BP.

XX AC AAV84287;

XX DT 12-APR-1999 (first entry)

XX DE LacZ reporter gene primer LacZPl.

XX KW Flk-1; endothelial growth factor receptor-2; VEGF; transcripti
 XX KW endothelium; enhancer; vascular disease; angiogenesis; cancer;
 XX KW diabetic retinopathy; rheumatoid arthritis; wound healing; vul
 XX KW atherosclerosis; tumour; neuronal disorder; therapy; diagnosis
 XX KW PCR; primer; lacZ; reporter gene; ss.

OS Synthesis

XX PN WO9855638-A.

XX PD 10-DEC-1998.

XX PF 03-JUN-1998; 98WO-EF003318.

XX PR 03-JUN-1997; 97EP-00108959.

XX PA (PLAC) MAX FLANCK GRS FOERDERUNG WISSENSCHAFTEN.

XX PI Breier G, Risau W, Roenicke V;

XX DR WPI; 1999-059915/05.

XX FT New recombinant DNA containing heterologous sequence controlle

XX PT endothelial cell specific regulator - from the Flk-1 gene, use

XX PT prevent or diagnose vascular disease, tumours, also to screen

XX PT transcriptional regulators.

XX PS Example 10; Page 48; 107pp; English.

XX CC This is the nucleotide sequence of primer LacZPl, which was us

XX CC primer LacZP2 (see AAV84288) in a PCR analysis for genotyping

XX CC knock-in mouse embryos, in which the lacZ gene was under contr

XX CC regulatory elements from the 5' untranslated region (5'-UTR, s

XX CC AAV84274) of the murine endothelial growth factor receptor-2 g

XX CC Complete vascular staining of Flk-1/lacZ knock-in embryos at E

XX CC indicated that the 5'-UTR is not essential for vascular expres

XX CC embryo proper. However, the 5'-UTR is required for expression

XX CC the yolk sac vasculature. The invention provides a new claimed

1 DNA comprising at least one regulatory sequence from an the Flk-1 gene that controls expression in endothelial cells, and which is linked to a heterologous DNA. Such constructs, comprising them, are used to produce pharmaceutical compositions for preventing and/or delaying vascular and tumorous diseases

0 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

71.4%; Score 20; DB 2; Length 20;

Similarity 100.0%; Pred. No. 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TCCTCTGCATGTCAGGTC 26

TCCTCTGCATGTCAGGTC 20

standard; DNA; 20 BP.

2 (first entry)

3 domain-containing fusion protein-related PCR primer 29.

tein; recombinase domain; signal peptide domain; gene function; port; recombinase recognition sequence; transgenic organism; combination system; site-specific integration; gene therapy; r; ss.

ad.

3-A2.

2.

1; 2001WO-EP012975.

0; 2000EP-00124629.

1; 2001EP-00109543.

1; 2001US-0311876P.

TEMIS PHARM GMBH.

Felder S, Schwenk F, Kueter-Luks B, Faust N;

319298/55.

on protein useful for recombining DNA molecules in eukaryotic recombinase protein which is linked to signal peptide domain its nuclear import of fusion protein in eucaryotic cells.

Page 131; 150pp; English.

ion comprises the amino acid and coding sequences of fusion that contain a recombinase domain and a signal peptide domain its nuclear import of the fusion protein in eukaryotic cells. proteins of the invention are useful for recombining the DNA of cells or organisms containing recombinase recognition for the recombinase domain of the fusion proteins. The fusion f the invention are useful for studying gene function at velopmental stages and for the creation of transgenic The C31-Int recombination system of the invention can be used re-specific integration of foreign DNA into the genome of cells (e.g. for gene therapy). The present DNA sequence a PCR primer that was used in the invention

0 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

71.4%; Score 20; DB 6; Length 20;

Similarity 100.0%; Pred. No. 52;

Matches 20; Conservative 0; Mismatches 0; Indels 0;

QY 7 ATCCTCTGCATGTCAGGTC 26

Db 1 ATCCTCTGCATGTCAGGTC 20

RESULT 4

ADB81355

ID ADB81355 standard; DNA; 20 BP.

XX ADB81355;

XX ADB81355;

DT 04-DEC-2003 (first entry)

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standard; DNA; 19 BP.

19 (first entry)

specific primer.

endothelial growth factor; VEGF; mouse; hypoxia;
disease; tumour; cancer; angiogenesis; wound healing; therapy;
PCR; primer; lacZ gene; ss.

la coli.

-Al.

38.

38; 98WO-EP003517.

37; 97EP-00109418.

LX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

Damert A, Plate K;

-080911/07.

inant DNA - contains sequence that regulates hypoxia-induced
t, used for, e.g. treatment and diagnosis of vascular disease.

: Page 34; 80pp; English.

specific primers (see AA82445 and AA82446) were used to
transfect GS9L cells following transfection with constructs
murine vascular endothelial growth factor (VEGF) gene
sequences as fusions to lacZ reporter genes. Experiments were
to determine hypoxia mediated expression of VEGF in vivo and in
invention relates to recombinant DNA molecules comprising
sequences of the VEGF gene, especially the 3' untranslated
region and promoter (see AA82440), being capable of
hypoxia inducible expression of a heterologous DNA in vivo.
abundant DNA molecules, vectors, host cells and transgenic
in be used to identify and develop compounds and methods for
treating, preventing and/or delaying a vascular or tumour

19 BP; 2 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

67.9%; Score 19; DB 2; Length 19;

Similarity 100.0%; Pred.No. 1.4e+02;

: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TCCTCTGCATGTCAGGTC 26

|||||

TCCTCTGCATGTCAGGTC 19

standard; DNA; 30 BP.

39 (first entry)

a cysteine protease PCR primer pro-pst1441.

protease; barley; transgenic plant; disease resistance;

prevention; treatment; infection; stress; temperature; drought;
wound; root-specific expression; antimicrobial; antistress;
anti-wounding; PCR primer; ss.

Synthetic.

Hordeum vulgare.

WO9910500-A1.

04-MAR-1999.

21-AUG-1998; 98WO-EP005339.

26-AUG-1997; 97DE-01037118.

22-JAN-1998; 98DE-01002384.

(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

Schlichter U, Steinbiss H, Antoniw J;

WPI; 1999-204668/17.

Nucleic acid encoding plant cysteine protease - that increase;
to injury and infection.

Example 6; Page 72; 81pp; German.

This invention describes a novel Hordeum vulgare cysteine protease
is used to produce transgenic plants with (a) increased or re-
expression of protease or (b) increased resistance to disease
(particularly prevention or treatment of infection) or other;
factors such as extreme temperatures, drought, salt or wound;
invention also describes a regulatory region which is used to
root-specific expression of heterologous DNA following infecti-
of roots. The products of the invention have antimicrobial, an-
and anti-wounding activity in plants

Sequence 30 BP; 4 A; 10 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 64.3%; Score 18; DB 2; Length 30;

Best Local Similarity 80.8%; Pred.No. 4e+02;

Matches 21; Conservative 0; Mismatches 5; Indels 0.

QY 3 CATCATCTCTGTCAGGTCAGGTCAT 28

|||||

Db 3 CATCTTCATCTGCAGGTCAGGTCCT 28

RESULT 7

ABN50202

ID ABN50202 standard; DNA; 60 BP.

XX AC ABN50202;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:;
Human; mouse; rat; splice transcript; detection; RNA transcrip-
splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

XX WO200210449-A2.

PD 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB001903.

XX 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;
257383/30.

olcoteid libraries comprising oligonucleotides which
hybridize to mRNAs transcribed from a transcription unit of a
cell for detecting tissue-, pathology-, and developmental-
genes.

SEQ ID NO 22950; 47pp; English.

The invention describes oligonucleotide libraries for detecting
mRNAs that populate a (sub-)transcriptome, where the (sub-
-)transcriptome comprises messenger RNAs transcribed from multiple
transcription units that populate a genome. The library comprises several
oligonucleotides, each capable of hybridizing selectively to a set of
mRNAs transcribed from a given transcription unit of the genome,
which are one or more messenger RNA splice variants. The
oligonucleotide libraries are useful for detecting mRNAs from a
sample, in expression profiling studies, in qualitatively or
quantitatively characterizing the corresponding transcriptome, and in
RNA transcripts and splice variants of human or animal
genes. The libraries may also be used as specialized mini-
libraries to detect transcripts of a sub-transcriptome under a particular
or pathological state, and so allowing the detection of tissue
or pathology-specific genes such as those genes only expressed in
a tissue under a specific pathological condition; to detect
specific genes; and to detect RNA transcripts and splice
variants; a transcriptome of a patient suffering from a particular
disease; ABN2753 to ABN59589 represent oligonucleotide sequences from
human and mice, which are used in the exemplification of the
invention. N.B. The sequence data for this patent did not form
part of the published specification, but was obtained in electronic format
from WIPO at ftp.wipo.int/pub/published_pct_sequences

BP; 13 A; 17 C; 15 G; 15 T; 0 U; 0 Other;

Similarity 62.1%; Score 17.4; DB 6; Length 60;

Conservative 77.8%; Pred. No. 8.1e+02;

Mismatches 0; Indels 6; Gaps 0;

ATCATCTCTTCGATGTCAGGTCTAT 28
|||||
CTCATGCTCTTCGATGTCAGGTCTCT 38

Standard; DNA; 40 BP.

(first entry)

ressible CpG deprived gene related oligo SEQ ID No 177.

Escherichia coli; expression; DNA vaccine; gene therapy; ds.

ad.

Al.

).

2001FR-00003274.

2001FR-00003274.

LA SARL.

715203/78.

PT Preparing gene with no cytosine methylation, useful e.g. for e
PT proteins in Escherichia coli, by selecting codons to avoid pre
XX CpG dinucleotides.

PS Disclosure; Fig 10a; 152pp; French.

XX The invention relates to a method for preparing a gene that la
CC is still expressible in Escherichia coli by synthesis of a pol
CC sequence, encoding a protein expressible in E. coli but lackin
CC codons NCG, CGN or NTA (N = any of A, C, G or T) or any codons
CC in C when the following codon starts with G. The CpG lacking g
CC especially useful as selection (antibiotic resistance) or mark
CC genes, but they (also CpG-free promoters, transcription units,
CC replication, plasmids and cells for replication of the plasmid
CC used for transformation, for biotechnological or medical purpo
CC they are particularly well suited for preparation of DNA vacci
CC in humans or animals. The polynucleotides of the invention can
CC for treating disorders by gene therapy. This polynucleotide se
CC represents an oligonucleotide relating to the Escherichia coli
CC expressible CpG gene of the invention

XX Sequence 40 BP; 5 A; 11 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 61.4%; Score 17.2; DB 6; Length 40;

Best Local Similarity 86.4%; Pred. No. 9.2e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGCATCATCTCTCGATGTCAT 22

|||||
Db 23 AGCACCATCTCTCGATGAC 2

RESULT 9

ABT12155

ID ABT12155 standard; DNA; 40 BP.

XX AC ABT12155;

DT 19-DEC-2002 (first entry)

XX E coli expressible CpG deprived gene related oligo SEQ ID No 1

XX CpG; Escherichia coli; expression; DNA vaccine; gene therapy;

XX Unidentified.

XX FR2821855-A1.

XX 13-SEP-2002.

XX 09-MAR-2001; 2001FR-00003274.

XX 09-MAR-2001; 2001FR-00003274.

XX (CAYL-) CAYLA SARL.

XX WPI; 2002-715203/78.

XX Preparing gene with no cytosine methylation, useful e.g. for e
PT proteins in Escherichia coli, by selecting codons to avoid pre
PT CpG dinucleotides.

PS Disclosure; Fig 10a; 152pp; French.

XX The invention relates to a method for preparing a gene that lac
CC is still expressible in Escherichia coli by synthesis of a pol
CC sequence, encoding a protein expressible in E. coli but lackin
CC codons NCG, CGN or NTA (N = any of A, C, G or T) or any codons
CC in C when the following codon starts with G. The CpG lacking ge
CC especially useful as selection (antibiotic resistance) or mark
CC genes, but they (also CpG-free promoters, transcription units,
CC replication, plasmids and cells for replication of the plasmid
CC used for transformation, for biotechnological or medical purpo

articularly well suited for preparation of DNA vaccines for use or animals. The polynucleotides of the invention can be used in disorders by gene therapy. This polynucleotide sequence an oligonucleotide relating to the *Escherichia coli* e CpG gene of the invention

0 BP; 14 A; 10 C; 9 G; 7 T; 0 U; 0 Other;

60.7%; Score 17; DB 6; Length 40;

ilarity 80.0%; Pred. No. 1.1e+03;

Conservative 0; Mismatches 5; Indels 0; Gaps 0;

TGATCTCTGCGATGTCAGTGCAT 28

|||||

CCACCTCTGCATGACAGTGAT 25

standard; DNA; 60 BP.

2 (first entry)

ced transcript detection oligonucleotide SEQ ID NO:21137.

se; rat; splice transcript; detection; RNA transcript;
iant; transcriptome; oligonucleotide library; ss.

ns.

9-A2.

2.

1; 2001WO-IB001903.

0; 2000US-0221607P.

1; 2001US-0287724P.

MPUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

257383/30.

ucleotide libraries comprising oligonucleotides which y hybridize to mRNAs transcribed from a transcription unit of a eful for detecting tissue-, pathology-, and developmental- enes.

SEQ ID NO 21137; 47pp; English.

t invention describes oligonucleotide libraries for detecting RNAs that populate a (sub-)transcriptome, where the (sub-)ome comprises messenger RNAs transcribed from multiple ion units that populate a genome. The library comprises several oxides, each capable of hybridizing selectively to a set of RNAs transcribed from a given transcription unit of the genome, des one or more messenger RNA splice variants. The oide libraries are useful for detecting mRNAs from a sample, in expression profiling studies, in qualitatively or vely characterizing the corresponding transcriptome, and in RNA transcripts and splice variants of human or animal ome. The libraries may also be used as specialised mini to detect transcripts of a sub-transcriptome under a particular or pathological state, and so allowing the detection of tissue ology-specific genes such as those genes only expressed in issue under a specific pathological condition; to detect tal specific genes; and to detect RNA transcripts and splice f a transcriptome of a patient suffering from a particular ABN27253 to ABN59589 represent oligonucleotide sequences from

CC rats, humans and mice, which are used in the exemplification c
CC present invention. N.B. The sequence data for this patent did
CC part of the printed specification, but was obtained in electr
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 14 A; 14 C; 18 G; 14 T; 0 U; 0 Other;

Query Match 60.0%; Score 16.8; DB 6; Length 60;

Best Local Similarity 75.0%; Pred. No. 1.5e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0;

QY 1 AGCATCATCTCTGCGATGTCAGTGCAT 28

|||||

Db 7 ACCATCATCCAGAGCTTGGCAGGTGAT 34

RESULT 11

AAQ51481

ID AAQ51481 standard; DNA; 29 BP.

XX

AC AAQ51481;

XX

DT 25-MAR-2003 (revised)

DT 16-MAY-1994 (first entry)

XX

DE Dengue virus sequence primer (pMAL-CRI/NS2-1 - DIR-NS2PM).

XX

KW Dengue haemorrhagic fever; DHF; dengue fever; DF; dengue shock
KW DSS; DEN1 polypeptides; Dengue Fever Virus Type; amplification
KW polymerase chain reaction; PCR; ss.

XX OS Synthetic.

XX WO9322440-A1.

XX 11-NOV-1993.

XX

PF 28-APR-1993; 93WO-CA000182.

XX

PR 29-APR-1992; 92GB-00009243.

XX

PA (UYSI-) UNIV SINGAPORE NAT.

XX

PI Tan Y, Fu J, Tan B, Yap E, Chan Y;

XX

DR WPI; 1993-368739/46.

XX

PT New Dengue virus type 1 strain - used to obtain prods. for det
PT diagnosis, vaccines and treatment involving virus.
PS Example 2; Page 18; 55pp; English.

XX

CC DEN1 virus, strain S275/90 was isolated from the serum of a de
CC haemorrhagic fever (DHF) patient. RNA was isolated from the vi
CC used to prepare cDNA encoding DEN1 polypeptides. Dengue Virus
CC prods. can be used for detection, diagnosis, vaccines (inactiv
CC or treatment of DEN1 infections. The sequences given in AAQ514
CC oligonucleotides used to prepare cDNA fragments corresp. to de
CC proteins, by PCR. (Updated on 25-MAR-2003 to correct PN field.

XX

SQ Sequence 29 BP; 9 A; 5 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 57.1%; Score 16; DB 2; Length 29;

Best Local Similarity 79.2%; Pred. No. 2.8e+03;

Matches 19; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGCATCATCTCTGCGATGTCAGG 24

|||||

Db 2 ATCAGAAATCTCTGCGAGGTGATG 25

RESULT 12

AAV39800

standard; cDNA; 42 BP.

1 (first entry)

1 tide SEQ ID NO:318 from WO9820166.

ometry; diagnosis; detection; biological sample; infection;
sease; chromosomal abnormality; identification; heredity;
organism; telomerase activity; oncogene mutation;
ific sequence; primer; ss.

12.

3.

1; 97WO-US020444.

1; 96US-00744481.
1; 96US-00744590.
1; 96US-00746036.
1; 96US-00746055.
1; 97US-00786988.
1; 97US-00787639.
1; 97US-00933792.
1; 97US-00947801.

1JENOM INC.

Tang K, Fu D, Siebert CW, Little DP, Higgins GS;
hamhoffer-Bemar B, Jurinke C, Van Den Boom D, Xiang G;

186975/25.

nucleic acid by mass spectrometric analysis - for detecting
ds, telomerase activity, oncogene mutations, or cancer-
sequences, for diagnosis of disease.

Page 335; 478pp; English.

has been developed for determining the sequence of a target
d. The process comprises: (i) generating at least two
F) from the target nucleic acid; and (ii) analysing F by mass
Y (MS). The sequences in AAV39483 to AAV39592 are specifically
mers for use in the mass spectrometric analysis of the above
e process is used to detect genetic diseases (e.g.
thalassaemia, Duchenne muscular dystrophy, Alzheimer's
stic fibrosis and many others) or chromosomal abnormalities
osition); infections and cancers; also for establishing
d heredity. Particular applications are diagnosis of
ma, detecting telomerase, determining family relationships and
bility, and in genetic fingerprinting. Compared with known
ng MS, this process requires fewer specific reagents and is
ed to automation. Extended primers are shorter; primer
s more efficient and the process allows detection of many
simultaneously. The present sequence represents an
tide from the present invention, which is not actually
within the specification, only within the sequence listing

1 BP; 12 A; 12 C; 9 G; 8 T; 0 U; 1 Other;

ilarity 57.1%; Score 16; DB 2; Length 42;

Conservative 79.2%; Pred. No. 3e+03;

Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CATCCTCTGCATGTCAGGTCA 27

|||||

CATCAACTGGAGATCAGGTCA 24

RESULT 13
AAV45436/c
ID AAV45436 standard; DNA; 30 BP.
XX
AC AAV45436;
XX
DT 18-JAN-1999 (first entry)
XX
DE Aspergillus oryzae pyrG gene PCR primer hemBdel.A.
XX
KW 5-Aminolevulinic acid synthase; hema gene; respiratory deficie
KW oxidative phosphorylation; PCR; primer; pyrG gene; ss.
XX
OS Synthetic.
OS Aspergillus oryzae.
XX
PN WO9841640-A1.
XX
PD 24-SEP-1998.
XX
PF 17-MAR-1998; 98WO-US005156.
XX
PR 17-MAR-1997; 97US-00819458.
XX
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO NORDISK BIOTECH INC.
XX
PI Jensen EB, Cherry JR, Elrod SL;
XX
DR WPI; 1998-521226/44.
XX
PT Production of polypeptide in respiratory-deficient cells trans;
PT construct - that complements the defect and encodes polypeptid
PT production of defective cells by disrupting gene essential for
PT phosphorylation.
XX
PS Example 9; Page 33; 57pp; English.
XX
CC Primer hemBdel.A and primer hemAΔel.A (see AAV45435) were used
CC amplification of a 4.1 kb fragment of the Aspergillus oryzae p
CC containing both 5' and 3' flanking DNA, including direct repea
CC to facilitate recombination and removal of a pyrG marker. The
CC was used in the construction of a hemAΔelA::pyrG allele (see
CC The invention relates to methods for producing polypeptides in
CC respiratory-deficient cells (e.g. haem-deficient cells). It in
CC transforming a respiratory-deficient cell with a first nucleic
CC sequence (e.g. hema gene) which complements the respiratory def
CC with a second nucleic acid sequence that encodes the respiratory de
CC culturing the cell, and isolating the polypeptide from the med
CC method of producing a respiratory-deficient cell, e.g. by disr
CC gene in a haem-deficient mutant cell, is also claimed
XX
SQ Sequence 30 BP; 10 A; 4 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 55.7%; Score 15.6; DB 2; Length 30;
Best Local Similarity 81.8%; Pred. No. 4.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0;
QY 1 AGCATTCATCCCTCTGCATGTCGA 22
DB 26 ATCGTCATCCCTCTGCTGTCGA 5
RESULT 14
ABN39943
ID ABN39943 standard; DNA; 60 BP.
XX
AC ABN39943;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:12

plasma; laminin; treatment; wound healing; solid tumour; scleroderma; myocardial angiogenesis; Crohn's disease; bilateral; arteriovenous malformation; rubecosis; cancer; tinopathy; arthritis; wound healing; peptic ulcer; r related disease; fracture; cat scratch fever; ds.

-A2.

; 99WO-US028897.

; 98US-00206059.

REMED INC.

J, Sim Kl;

12290/35.

nesis-inhibiting protein receptors, useful in methods for seases and processes that are mediated by angiogenesis, such mers, psoriasis, scleroderma and myocardial angiogenesis.

ge 96; 100pp; English.

ion relates to angiogenesis-inhibiting protein receptors, and uences encoding them. Angiogenesis is the generation of new ls into a tissue, and normally occurs in wound healing, foetal al development and the formation of the corpus luteum, and placenta. Angiostatin is a protein (see AAB16450 and involved in angiogenesis, and has an amino acid sequence that of a plasminogen fragment (see murine plasminogen Angiostatin has the ability to inhibit angiogenesis.

is also an angiogenesis inhibiting protein (see AAB16451 and Sequences AAB68242 and AAB16522 represent coding and protein f human laminin. Laminin is an angiostatin binding protein, the peptides of the invention share homology with regions of ptides AAB16452-B16521 (excluding AAB16490) are the s-inhibiting protein receptor fragments of the invention. The nd either angiostatin or endostatin and can be used in methods g diseases and processes that are mediated by angiogenesis, id tumours, psoriasis, scleroderma, myocardial angiogenesis, ease, cerebral collaterals, arteriovenous malformations, iabetic retinopathy, arthritis, wound healing, peptic ulcers, r related diseases, fractures, placenta and cat scratch are useful for the detection and prognosis of cancer. DNA .628204-A628241 encode the peptides of the invention

BP; 5 A; 10 C; 9 G; 9 T; 0 U; 0 Other;

54.3%; Score 15.2; DB 3; Length 33;

ilarity 85.0%; Pred. No. 6.4e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CCATCATCTGTCATGGT 20

|||||

CCCTCATCTGTCATGGT 24

andard; DNA; 39 BP.

l (first entry)

; peptide analogue coding sequence SEQ ID NO: 23.

;5; glutamic acid decarboxylase; type 1 diabetes;

KW insulin dependent diabetes mellitus; IDDM; analogue; ds.
XX Homo sapiens.
OS WO200113934-A1.
PN 01-MAR-2001.
PD 17-AUG-2000; 2000WO-US022661.
PF 23-AUG-1999; 99US-00379211.
PR (VIRG-) VIRGINIA MASON RES CENT.
PA Nepom GT, Masewicz S, Nepom BS;
PI WPI; 2001-226589/23.
DR Novel peptides and peptide analogs designed from human pancreatic
PT beta cell autoantigen GAD65, useful for the treatment and preve
PT type 1 diabetes, pre-diabetes or recurring autoimmunity.
XX Disclosure; Page 53; 57pp; English.

CC The present invention provides a number of peptide analogues of
CC GAD65 protein (the 65 kDa isoform of glutamic acid decarboxylase
CC are useful as they antagonise autoimmune T cell activation in
CC GAD65 and prevent type 1 diabetes (also known as insulin depend
CC diabetes mellitus or IDDM). They can thus be used in the treat
CC diabetes, as well as in the prevention of its occurrence in an
CC with pre-IDDM. The present sequence is an example of a coding s
CC a peptide analogue of the invention

XX SQ Sequence 39 BP; 10 A; 12 C; 7 G; 10 T; 0 U; 0 Other;

Query Match

Best Local Similarity 54.3%; Score 15.2; DB 5; Length 39;

Matches 17; Conservative 85.0%; Pred. No. 6.6e+03;

Mismatches 3; Indels 0;

OY 8 TCCTCTGTCATGGTCAGGTCA 27

|||||

Db 5 TCTTCGTCATGGTCATGTCA 24

RESULT 18

AAV20388

ID AAV20388 standard; DNA; 56 BP.

XX AAV20388;

AC AAV20388;

XX 26-JUN-1998 (first entry)

XX Primer 5 for human immunity related factor cDNA.

DE Lymph node; human; immunity related factor; research; treatment

KW immune disease; infectious disease; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX JPI0072495-A.

PN 17-MAR-1998.

PD 11-JUN-1997; 97JP-00153218.

XX 13-JUN-1996; 96JP-00152362.

XX (ASAH) ASAH KOGYO KK.

PA WPI; 1998-234766/21.

XX Immunity related factor - useful in the treatment of immune re.

XX

PT

Page 11: 21pp; Japanese.

; BP: 12 A: 13 C: 9 G: 22 T: 0 U: 0 Other:

GCATCATCCTCTGTCATGGTCAAGTCA T 28
||||| ||| ||| ||| |||
TCATCATCATCTTTATAATCGGGTCT 42

2 (first entry)

7-A2.

10-200015-0206920P.

Wittman V, Weidanz JA, Burkhardt M, Card KF, Tal R;
Wong HC;

ing modulators of T cell receptor (TCR) and major histocompatibility complex (MHC) antigen immune complexes, useful for immunologic disorders, by determining if a test compound alters TCR-MHC binding.

ices given in AI172184-86 are primers which were used in the murine CD4 and CD4 delta CM sequences. The resulting sequences in the generation of murine T cells carrying recombinant T cell and recombinant CD4 molecules. These cells were used in the invention to determine whether the inventive complexes an immune complex. The method may be used for providing high screening assays for detecting and identifying compositions or which are useful for modulating an immune response, especially al. The compounds are particularly useful for treating immune e.g. autoimmune diseases or allergies

54 3% Score 15.2: DB 6: Length 58:

Similarity 85.0%; Pred. No. 7e+03;

QY	6	CATCCTCTGCATGGT	25
DB	53	CATCCTCTGGTGTGT	34

RESULT 20
ABN47436

ABN4/438
TD ARN47436 standard: DNA: 60 BP.

XX
AC
APR 14 7 12 6.[illegible][illegible]

XX Human; mouse; rat; splice transcript; detection; RNA transcript
KW splice variant; transcriptome; oligonucleotide library; ss.
XX splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

AA
PN
W0200270449-A2.

XX
07-338-3002

XX
20
20

- 30 -

[illegible]

PR 02-MAY-2001; 2001US-0287724P.

PA (COMP-) COMPUGEN INC.

Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

WPT: 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcrip-
PT tase gene, useful for detecting tissue-, pathology-, and develop-
PT mentally-regulated genes.

XX
PS
Example 1: SEQ ID NO 20184: 47pp: English.

The present invention describes oligonucleotide libraries for messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises oligonucleotides, each capable of hybridising selectively to a messenger RNA transcribed from a given transcription unit of which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitative and quantitative characterising the corresponding transcriptome, detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised libraries to detect transcripts of a sub-transcriptome under a biological or pathological state, and so allowing the detection and/or pathology-specific genes such as those genes only expressed in a specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN5989 represent oligonucleotide sequences in rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form from the patent applicant's patent/copyrighted computer sequences.

XX
SC
Sentence 60 BP. 12 A. 16 C. 14 G. 18 T. 0 U. 0 Other;

Country	Match	EA 3%	Score	15.2:	DB 6:	Length	60%
---------	-------	-------	-------	-------	-------	--------	-----

Best Local Similarity	85.0%	Pred. NO. 7.1e+03;	Indels
Conservative	17.0	Mismatches	3:
Indels	0:		

ATCCTGTCAGTGCAGGT 25
|||||
ATCCACTGCTTGGTCAGGT 37

-andard; DNA; 25 BP.

3 (first entry)

array DNA oligonucleotide SEQ ID NO 9236.

robe; expressed sequence tag; microarray; gene expression;
iation; biallelic marker; polymorphism; human;
ies comparison.

1S.

10-A1.

3.

2; 2002US-00098263.

1; 2001US-0276759P.

FYMETRIX INC.

2;

357953/53.

of nucleic acid probes, useful for in situ hybridization, in
Northern or dot-blot hybridization to identify or detect the
r specific mutations of any gene.

EQ ID NO 9236; 9pp; English.

ion discloses a microarray comprising a plurality of nucleic
s including one of 2,018,500 fully defined sequences, or its
tch, perfect mismatch, antisense match or antisense mismatch.
sed is a method of gene expression analysis. The array is used
ing gene expression levels by hybridisation to a DNA library,
s of genetic variation or in hybridisation of tag-labelled
The nucleic acid probes are specifically designed for analysis
t one target sequence. The method of analysis comprises
g at least one or more nucleic acids to at least two or more
id probes and detecting the hybridisation. The nucleic acid
attached to a solid support. The analysis comprises monitoring
sion levels, identifying biallelic markers or polymorphisms,
members of a gene and a cross-species comparison. Each of the
ids further comprises a tag sequence. The array of nucleic acid
useful in situ hybridisation, in Southern, Northern or dot-
disation to identify or detect the sequence or specific
of any gene, in mapping the 5' termini of mRNA molecules by
ensions or in screening cDNA or genomic libraries or subclones
onal subclones containing segments of DNA that have been
nd previously sequenced. The sequence presented is one of the
id probes incorporated in the microarray. Note: The sequence
his patent can also be obtained in electronic format directly
at seqdata.uspto.gov/sequence.html

5 BP; 4 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

53.6%; Score 15; DB 8; Length 25;
milarity 78.3%; Pred. No. 7.4e+03;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ATCCTGTCAGTGCAGGT 28

Db 3 CGTCTCTTCATGTCAGGCAT 25

RESULT 22

AAF8886/c

ID AAF8886 standard; DNA; 41 BP.

XX

AC AAF8886;

XX

DT 07-JAN-2003 (first entry)

XX

DE Aldehyde/ketone reductase 8.8 probe SEQ ID 9.

XX

KW Aldehyde/ketone reductase 8.8; malignant tumour; haemopathy;
human immunodeficiency virus; HIV infection; immunological dis

KW

inflammation; probe; detection; ss.

XX

OS Unidentified.

XX

PN CN1352260-A.

XX

PD 05-JUN-2002.

XX

PF 10-NOV-2000; 2000CN-00127325.

XX

PR 10-NOV-2000; 2000CN-00127325.

XX

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-714449/78.

XX

PT New polypeptide-aldehyde/ketone reductase 8.8 and polynucleoti
encoding such polypeptide.

XX

PS Example 6; Page 19 (Disclosure); 32pp; Chinese.

XX

CC This invention describes a novel aldehyde/ketone reductase, 8.
polynucleotides for encoding this polypeptide and a DNA recomb
process to produce the polypeptide. The invention also disclos
the polypeptide in treating various diseases, such as malignan
CC haemopathy, human immunodeficiency virus (HIV) infection, immu
diseases and various inflammations. This sequence represents a
CC in the detection of the aldehyde/ketone reductase 8.8 describe
disclosure of the invention

XX

SQ Sequence 41 BP; 7 A; 9 C; 16 G; 9 T; 0 U; 0 Other;

Query Match 53.6%; Score 15; DB 6; Length 41;

Best Local Similarity 78.3%; Pred. No. 8.1e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0;

QY 3 CATCATCTCTGTCAGTGCAGGT 25

Db 29 CCTCAACCTGGCATGTCAGGT 7

RESULT 23

AAH43442

ID AAH43442 standard; DNA; 44 BP.

XX

AC AAH43442;

XX

DT 04-DEC-2001 (first entry)

XX

DE Primer J 903 p7H6.

XX

KW Polymerase chain reaction; primer; amplify; PCR; hepatitis C v
NS2/3 protease; homodimer; autoproteolytic activity; inhibit;

XX

OS Synthetic.

I-A2.

2001WO-1B000527.

2000GB-00006537.

RICERCHIE BIOL MOLECOLARE ANGELETTI.

C. Pallaro M, Lahm A;

390054/66.

is C virus (HCV) NS2/3 protease fragment having lytic activity when present as homodimer, useful for modulators of HCV NS2/3 protease that are useful for treating

Page 43; 80pp; English.

ses given in AH43431-46 are primers which were used to amplify fragments of hepatitis C virus (HCV) NS2/3 protease. The cDNA's encode fragments which have as the N-terminal, an amino is at position 903-913 in HCV NS2/3 protease precursor and as inal an amino acid that is at position 1206-1657 in HCV NS2/3 reursor. The protein fragments, in homodimeric form, have lytic activity. They are useful for testing the ability of an odulate activity of HCV NS2/3 protease which involves bringing nt into contact with the protein fragment or a homodimer and g formation of the homodimer and/or HCV NS2/3 protease The modulator compounds identified using this method modulate, inhibit, the autolytic activity of NS2/3 precursor and are useful for treating HCV infection or for manufacturing a n, medicament or drug for treating HCV infection

4 BP; 11 A; 12 C; 10 G; 11 T; 0 U; 0 Other;

53.6%; Score 15; DB 4; Length 44;

ilarity 78.3%; Pred. No. 8.2e+03;

Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CATCATCTCTGCGATGTCAGG 24

CATCATCATCATCATCATCATG 24

standard; DNA; 60 BP.

2 (first entry)

ced transcript detection oligonucleotide SEQ ID NO:31738.

use; rat; splice transcript; detection; RNA transcript;

iant; transcriptome; oligonucleotide library; ss.

ans.

19-A2.

32.

31; 2001WO-1B001903.

30; 2000US-0221607P.

31; 2001US-0287724P.

OMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription
PT genome, useful for detecting tissue-, pathology-, and developm
PT specific genes.
XX Example 1; SEQ ID NO 31738; 47pp; English.
XX The present invention describes oligonucleotide libraries for
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC transcriptome comprises messenger RNAs transcribed from multi
CC transcription units that populate a genome. The library compri
CC oligonucleotides, each capable of hybridising selectively to a
CC messenger RNAs transcribed from a given transcription unit of
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from
CC biological sample, in expression profiling studies, in qualita
CC quantitatively characterising the corresponding transcriptome,
CC detecting RNA transcripts and splice variants of human or anim
CC transcriptomes. The libraries may also be used as specialised
CC biological or pathological state, and so allowing the detectio
CC - and pathology-specific genes such as those genes only expres
CC specific tissue under a specific pathological condition; to de
CC developmental specific genes; and to detect RNA transcripts an
CC variants of a transcriptome of a patient suffering from a part
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequ
CC rats, humans and mice, which are used in the exemplification o
CC present invention. N.B. The sequence data for this patent did
CC part of the printed specification, but was obtained in electio
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 60 BP; 13 A; 15 C; 17 G; 15 T; 0 U; 0 Other;

Query Match 53.6%; Score 15; DB 6; Length 60;

Best Local Similarity 78.3%; Pred. No. 8.6e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0;

QY 2 GCATCATCTCTGCGATGTCAGG 24

Db 25 GCATCACCATCTTCATGTCAGG 3

RESULT 25

ABN59110/c

ID ABN59110 standard; DNA; 60 BP.

XX AC ABN59110;

XX 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:3

XX Human, mouse; rat; splice transcript; detection; RNA transcrip

XX splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-1B001903.

XX 28-JUL-2000; 2000US-0221607P.

XX 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

XX

Wasserman A, Mintz E, Mintz L, Faigler S;

57383/30.

cleotide libraries comprising oligonucleotides which hybridize to mRNAs transcribed from a transcription unit of a full for detecting tissue-, pathology-, and developmental-nes.

SEQ ID NO 31858; 47pp; English.

invention describes oligonucleotide libraries for detecting mRNAs that populate a (sub-)transcriptome, where the (sub-)ome comprises messenger RNAs transcribed from multiple on units that populate a genome. The library comprises several itides, each capable of hybridizing selectively to a set of mRNAs transcribed from a given transcription unit of the genome, ies one or more messenger RNA splice variants. The ide libraries are useful for detecting mRNAs from a sample, in expression profiling studies, in qualitatively or rely characterizing the corresponding transcriptome, and in rna transcripts and splice variants of human or animal mes. The libraries may also be used as specialized mini o detect transcripts of a sub-transcriptome under a particular or pathological state, and so allowing the detection of tissue ology-specific genes such as those genes only expressed in issue under a specific pathological condition; to detect al specific genes; and to detect RNA transcripts and splice a transcriptome of a patient suffering from a particular BN27253 to ABN59589 represent oligonucleotide sequences from s and mice, which are used in the exemplification of the ention. N.B. The sequence data for this patent did not form a printed specification, but was obtained in electronic format om WIPO at ftp.wipo.int/pub/published_pct_sequences

) BP; 13 A; 15 C; 17 G; 15 T; 0 U; 0 Other;

ilarity 53.6%; Score 15; DB 6; Length 60;

Conservative 0; Mismatches 5; Indels 0; Gaps 0;

TATCATCTCTCGATGGTCAGG 24

||||| ||||| ||||| ||||| |||||

TATCACCATCTTCATGTTGAGG 3

standard; DNA; 25 BP.

3 (first entry)

array DNA oligonucleotide SEQ ID NO 19509.

robe; expressed sequence tag; microarray; gene expression; riation; biallelic marker; polymorphism; human; ies comparison.

ns.

10-A1.

3.

2; 2002US-00098263.

1; 2001US-0276759P.

FYMETRIX INC.

IP;

XX

WPI; 2003-567953/53.

XX

New array of nucleic acid probes, useful for in situ hybridizat PT Southern, Northern or dot-blot hybridization to identify or del sequence or specific mutations of any gene.

XX

Claim 1; SEQ ID NO 19509; 9pp; English.

XX

The invention discloses a microarray comprising a plurality of CC acid probes including one of 2,018,500 fully defined sequences. CC perfect match, antisense match or antisense match or antisense match. Also disclosed is a method of gene expression analysis. The ar CC in monitoring gene expression levels by hybridisation to a DNA CC in analysis of genetic variation or in hybridisation of tag-lal CC compounds. The nucleic acid probes are specifically designed f CC of at least one tag sequence. The method of analysis compris CC hybridising at least one or more nucleic acids to at least two CC nucleic acid probes and detecting the hybridisation. The nucle CC probes are attached to a solid support. The analysis comprises CC gene expression levels, identifying biallelic markers or polym CC or family members of a gene and a cross-species comparison. Eac CC nucleic acids further comprises a tag sequence. The array of m CC blot hybridisation in situ hybridisation, in Southern, Northern CC blot hybridisation to identify or detect the sequence or speci CC mutations of any gene, in mapping the 5' termini of mRNA molec CC primer extensions or in screening cDNA or genomic libraries or CC for additional subclones containing segments of DNA that have l CC isolated and previously sequenced. The sequence presented is o CC nucleic acid probes incorporated in the microarray. Note: The CC data for this patent can also be obtained in electronic format CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 6 A; 7 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 52.9%; Score 14.8; DB 8; Length 25;

Best Local Similarity 88.9%; Pred. No. 9e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 9 CCTCTGCATGGTCAGGTC 26

||||| ||||| ||||| ||||| |||||

Db 25 CCTCTGGATGGTCAGGTC 8

RESULT 27

AAA79182/c

ID AAA79182 standard; DNA; 31 BP.

XX AAA79182;

XX 20-NOV-2000 (first entry)

Human genomic DNA polymorphic site sequence tag SEQ ID NO:552.

Human; genomic DNA; polymorphism; genome; allele-specific; pri hybridisation; polymorphic site; forensic; paternity testing; phenotypic trait; genetic analysis; genetic mapping; ds.

OS Homo sapiens.

XX EF1024200-A2.

XX 02-AUG-2000.

XX 26-JAN-2000; 2000EP-00250023.

XX 27-JAN-1999; 99US-00238402.

XX (AFFY-) AFFYMETRIX INC.

XX Patil N, Shah N, Warrington JA;

XX WPI; 2000-500198/45.

XX

ic polymorphic nucleic acid segments, allele specific primers and methods of analysis, useful for e.g. forensics, paternity genetic mapping,.

age 20; 141pp; English.

; invention describes a nucleic acid segment of 10-100 bases chosen from one of 632 fragments (AAA78631 to AAA79262), segment comprises a polymorphic site or an immediately adjacent complement of the segment. Also described are: (1) an allele oligonucleotide that hybridises to a segment of the novelty; related nucleic acid comprising a sequence of the novelty where phic site within the sequence is occupied by a base other than ace base indicated in the specification; and (3) analysing a id, comprising obtaining a nucleic acid from an individual, and y a base occupying any one of the polymorphic sites of the he nucleic acid segments and method can be used to analyse an s nucleic acid sequences for the presence of polymorphisms. The also be used to test for a disease phenotype and correlate the f the phenotype with a particular polymorphism. The presence of 2 sites are useful for, e.g. forensics, paternity testing, a of polymorphisms with phenotypic traits and for genetic phenotypic traits. AAA78631 to AAA79262 represent sequence nan genomic DNA fragments containing polymorphic sites. The ying the polymorphic site is indicated using IUPAC-IUB re

1 BP; 8 A; 9 C; 9 G; 4 T; 0 U; 1 Other;

ilarity 52.9%; Score 14.8; DB 3; Length 31;

Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GCATCATCTCTGTCATGTT 20

|||||:|||||
GCTCTGTCCTGTCATGTT 3

standard; RNA; 50 BP.

0 (first entry)

embrane-binding RNA molecule #6.

; antitumour; cellular membrane; binding; liposome; SELEX; ss;
; Evolution of Ligands by Exponential enrichment; permeability.

A1.

19.

19; 99WO-US011237.

18; 98US-0086492P.

19; 99US-00315886.

NIV TECHNOLOGY CORP.

1, Yarus M;

-072599/06.

ucleic acids to phospholipid membranes, particularly for
membrane permeability.

; Fig 3; 67pp; English.

XX
CC The invention relates to a method for binding nucleic acids to
CC by combining a composition containing at least one nucleic acid
CC phospholipid membrane preparation and isolating the membrane-b
CC nucleic acid. Isolation of membrane bound nucleic acid is by a
CC Evolution of Ligands by Exponential enrichment (SELEX) method.
CC especially comprises the generation of a 95 bp oligonucleotide
CC randomised central 50 bp flanked by primer binding sites (see
CC 247154). The oligonucleotides are transcribed from an upstream
CC promoter and the resultant RNA is combined with phosphatidylch
CC liposomes to isolate the best binding sequences. The method is
CC used to isolate RNA molecules able to alter the permeability,
CC channel formation, of membranes, e.g. for treatment of ion-cha
CC diseases such as Liddle's syndrome, cystic fibrosis or pulmona
CC membranes, e.g. to assess cellular function, to analyze change
CC membrane structure and fluidity, or to differentiate between t
CC cells. The nucleic acids may also be used to target effector m
CC (e.g. toxins, growth factors, cytokines, ribozymes, or targetin
CC such as antibodies) for treatment or diagnosis, e.g. of tumour
CC pathogenic organisms. This sequence represents an example of a
CC binding RNA oligonucleotide

XX
SQ Sequence 50 BP; 7 A; 9 C; 14 G; 0 T; 20 U; 0 Other;

Query Match 52.9%; Score 14.8; DB 3; Length 50;

Best Local Similarity 46.2%; Pred. No. 1e+04;

Matches 12; Conservative 7; Mismatches 7; Indels 0;

QY 1 AGCATCATCTCTGTCATGTCAGTTC 26

|||||:|||||
7 AUCUUAUUCUGUGCGUGGAGGUC 32

RESULT 29

ABZ01817

ID ABZ01817 standard; DNA; 50 BP.

XX AC ABZ01817;

XX DT 09-JAN-2003 (first entry)

XX DE Human leukocyte gene expression profiling probe SEQ ID NO 1808

XX KW T7; leukocyte; gene expression profiling; allograft rejection;
XX KW atherosclerosis; congestive heart failure; systemic lupus eryt
XX KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infecti
XX KW ss.

XX OS Homo sapiens.

XX PN WO200257414-A2.

XX PD 25-JUL-2002.

XX PF 22-OCT-2001; 2001WO-US047856.

XX PR 20-OCT-2000; 2000US-0241994P.

XX PR 08-JUN-2001; 2001US-0296764P.

XX PA (BIOC-) BIOCARDIA INC.

XX PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phil
XX PI Ly N, Woodward R, Quertemous T, Johnson F;

XX DR WPI; 2002-635525/68.

XX PT New system for leukocyte expression profiling, diagnosing a di
XX PT monitoring (the rate of) progression of a disease, e.g. ather
XX PT or congestive heart failure, comprises diagnostic oligonucleot
XX PS Claim 1; Page 383; Opp; English.

ion relates to a system for detecting gene expression, which one or two isolated DNA molecules that detect expression of a gene corresponds to any of 8143 oligonucleotides (AB08152) each having 50 base pairs (bp). The system is useful for gene expression profiling. It is particularly useful for a disease, monitoring (rate of) progression of a disease, therapeutic outcome, determining prognosis for a patient, disease complications in an individual or monitoring response in an individual. The diseases include cardiac allograft kidney allograft rejection, liver allograft rejection, rosacea, congestive heart failure, systemic lupus erythematosus, arthritis, osteoarthritis or cytomegalovirus infection

BP; 10 A; 7 C; 12 G; 21 T; 0 U; 0 Other;

ilarity 52.9%; Score 14.8; DB 6; Length 50;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TGCGATGTCAGGTCAT 28
|||||
TGCGATGTCAGGTCAT 40

andard; DNA; 51 BP.

1 (first entry)

at SNP containing nucleic acid SEQ:1253.

ple nucleotide polymorphism; SNP: genome; gene therapy; arapy; vaccine; probe; diagnostic assay; detection; ni; restorative therapy; polymorphic; ds.

1s.

1-A2.

1.

0; 2000WO-US032758.

9; 99US-0168138P.

0; 2000US-00726173.

RAGEN CORP.

A, Leach M;

356160/37.

c nucleic acid sequences, useful in genetic testing and

age 437; 2653pp; English.

o AAT79867 represent isolated human polymorphic polynucleotide (I), which contain single nucleotide polymorphisms (SNPs). o AAM53329 represent peptides related to human polymorphic tide sequences. The sequences can be used in gene and protein nd in vaccine production. (I) and the polypeptides encoded by e used in the prevention, diagnosis and treatment of diseases with inappropriate expression of polymorphic polypeptides. For I) may be used to treat disorders by rectifying mutations or in a patient's genome that affect the activity of polypeptides of polypeptide. Additionally, (I) and its complementary may also be used as DNA probes in diagnostic assays to detect tate the presence of similar nucleic acids in samples, and

CC therefore which patients may be in need of restorative therapy
CC polypeptides encoded by (I) may be used as antigens in the pro
CC antibodies specific for polymorphic polypeptides. The antibody
CC be used to down regulate expression and activity. The antibody
CC be used as diagnostic agents for detecting the presence of pol
CC polypeptides in samples

XX Sequence 51 BP; 7 A; 13 C; 19 G; 12 T; 0 U; 0 Other;

Query Match 52.9%; Score 14.8; DB 4; Length 51;

Best Local Similarity 73.1%; Pred. No. 1e+04;

Matches 19; Conservative 0; Mismatches 7; Indels 0;

QY 1 AGCATCACCCTCTGCATGTCAGGTC 26
|||||
Db 12 AGCAGTCTTCTCGGGTCGTCAGGTC 37

RESULT 31

ACA15508/c

ID ACA15508 standard; DNA; 53 BP.

XX ACA15508;

XX 27-OCT-2003 (revised)

DT 19-JUN-2003 (first entry)

XX

DE Prokaryotic essential gene antisense oligonucleotide #3378.

XX Antisense; ss; prokaryotic essential gene; cell proliferation;
XX drug design.

XX Archaea.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 23-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zysk

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu H

XX

DR WPI; 2003-029926/02.

XX New antisense nucleic acids, useful for identifying proteins o
PT for homologous nucleic acids required for cellular proliferati
PT isolate candidate molecules for rational drug discovery progra

PS Claim 1; SEQ ID NO 3378; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising a
CC the 6213 antisense sequences given in the specification where
CC of the nucleic acid inhibits proliferation of a cell. Also inc
CC (1) a vector comprising a promoter operably linked to the nucl
CC encoding a polypeptide whose expression is inhibited by the an
CC nucleic acid; (2) a host cell containing the vector; (3) an is
CC polypeptide or its fragment whose expression is inhibited by t
CC antisense nucleic acid; (4) an antibody capable of specificall
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting
CC proliferation or the activity of a gene in an operon required
CC proliferation; (7) identifying a compound that influences the
CC the gene product or that has an activity against a biological
CC required for proliferation, or that inhibits cellular prolifer
CC identifying a gene required for cellular proliferation or the

which a proliferation-required gene or its gene product lies on which the test compound that inhibits proliferation of an sts; (9) manufacturing an antibiotic; (10) profiling a activity; (11) a culture comprising strains in which the gene overexpressed or underexpressed; (12) determining the extent of the strains is present in a culture or collection of r (13) identifying the target of a compound that inhibits the ion of an organism. The antisense nucleic acids are useful for g proteins or screening for homologous nucleic acids required ar proliferation to isolate candidate molecules for rational very programs, or for screening homologous nucleic acids or proliferation in cells other than *S. aureus*, *S. typhimurium*, iae or *P. aeruginosa*. The present sequence is one of the 6213 sequences of the invention. Note: The sequence data for this not form part of the printed specification, but was obtained nic format directly from WIPO at nt/pub/published_pct_sequences. (Updated on 27-OCT-2003 to e OS field)

3 BP; 7 A; 13 C; 12 G; 21 T; 0 U; 0 Other;

52.9%; Score 14.8; DB 7; Length 53;

milarity 73.1%; Pred. No. 1e+04; 7; Indels 0; Gaps 0;

Conservative 0; Mismatches 7; Indels 0; Gaps 0;

GCATCATCTCTGTCATGTCAGTTC 26
||||| ||||| ||||| |||||
GCATCAAGCTCAGCAAGTGAAGTC 3

standard; DNA; 60 BP.

12 (first entry)

ded transcript detection oligonucleotide SEQ ID NO:18696.

use; rat; splice transcript; detection; RNA transcript;
nant; transcriptome; oligonucleotide library; ss.

ms.

19-A2.

12.

01; 2001WO-IB001903.

00; 2000US-0221607P.

01; 2001US-0287724P.

OMPUGEN INC.

, Wasserman A, Mintz E, Mintz L, Faigler S;

-257383/30.

nucleotide libraries comprising oligonucleotides which ly hybridize to mRNAs transcribed from a transcription unit of a seful for detecting tissue-, pathology-, and developmental- genes.

; SEQ ID NO 18696; 47pp; English.

nt invention describes oligonucleotide libraries for detecting RNAs that populate a (sub-)transcriptome, where the (sub-)ptome comprises messenger RNAs transcribed from multiple tion units that populate a genome. The library comprises several etides, each capable of hybridising selectively to a set of RNAs transcribed from a given transcription unit of the genome,

CC which encodes one or more messenger RNA splice variants. The CC oligonucleotide libraries are useful for detecting mRNAs from CC biological sample, in expression profiling studies, in qualita CC quantitatively characterising the corresponding transcriptome, CC detecting RNA transcripts and splice variants of human or anim CC transcriptomes. The libraries may also be used as specialised CC libraries to detect transcripts of a sub-transcriptome under a CC biological or pathological state, and so allowing the detecti CC - and pathology-specific genes such as those genes only expres CC specific tissue under a specific pathological condition; to de CC developmental specific genes; and to detect RNA transcripts an CC variants of a transcriptome of a patient suffering from a part CC disorder. ABN27253 to ABN59589 represent oligonucleotide seque CC rats, humans and mice, which are used in the exemplification c CC present invention. N.B. The sequence data for this patent did CC part of the printed specification, but was obtained in electr CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences CC
SQ Sequence 60 BP; 16 A; 21 C; 9 G; 14 T; 0 U; 0 Other;

Query Match 52.9%; Score 14.8; DB 6; Length 60;

Best Local Similarity 73.1%; Pred. No. 1.1e+04;

Matches 19; Conservative 0; Mismatches 7; Indels 0;

Qy 3 CATCATCTCTGTCATGTCAGTTCAT 28

Db 2 CTTTCATCCACTCCATGCTCAGCAGT 27
||||| ||||| ||||| |||||

RESULT 33

ABN43493/C

ID ABN43493 standard; DNA; 60 BP.

XX AC ABN43493;

XX DT 15-JUL-2002 (first entry)

XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:1

XX KW Human; mouse; rat; splice transcript; detection; RNA transcrip

XX KW splice variant; transcriptome; oligonucleotide library; ss.

XX OS Homo sapiens.

XX FN WO200210449-A2.

XX PD 07-FEB-2002.

XX PF 20-JUL-2001; 2001WO-IB001903.

XX PR 28-JUL-2000; 2000US-0221607P.

XX PR 02-MAY-2001; 2001US-0287724P.

XX PA (COMP-) COMPUTEN INC.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX DR WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides whi PT selectively hybridize to mRNAs transcribed from a transcripti PT genome, useful for detecting tissue-, pathology-, and developi PT specific genes.

XX PS Example 1; SEQ ID NO 16241; 47pp; English.

XX The present invention describes oligonucleotide libraries for CC messenger RNAs that populate a (sub-)transcriptome, where the CC)transcriptome comprises messenger RNAs transcribed from mult CC transcription units that populate a genome. The library compr CC oligonucleotides, each capable of hybridising selectively to CC messenger RNAs transcribed from a given transcription unit of CC which encodes one or more messenger RNA splice variants. The CC

otide libraries are useful for detecting mRNAs from a sample, in expression profiling studies, in qualitatively or vely characterizing the corresponding transcriptome, and in RNA transcripts and splice variants of human or animal omes. The libraries may also be used as specialised mini to detect transcripts of a sub-transcriptome under a particular or pathological state, and so allowing the detection of tissue ology-specific genes such as those genes only expressed in issue under a specific pathological condition; to detect tal specific genes; and to detect RNA transcripts and splice ABN27253 to ABN59589 represent oligonucleotide sequences from ns and mice, which are used in the exemplification of the vention. N.B. The sequence data for this patent did not form e printed specification, but was obtained in electronic format rom WIPO at ftp.wipo.int/pub/published_pct_sequences

0 BP; 19 A; 16 C; 10 G; 15 T; 0 U; 0 Other;

milarity 52.9%; Score 14.8; DB 6; Length 60;

milarity 73.1%; Pred. No. 1.1e+04; Mismatches 0; Gaps 0; Conservative 0; Indels 0;

CATCATCCTCTGCATGTCAGGTCA 27

||||| ||||| ||||| |||||

CATCATCACTGGATAGGAATTCA 20

standard; DNA; 22 BP.

3 (first entry)

DNA PCR primer #13.

X; inflammatory disorder; demyelination disease; stroke; rder; infection; cardiomyopathy; atherosclerosis; acne; on; pancreatitis; Von Hippel-Lindau; endometriosis; fertility; a; cirrhosis; inflammatory bowel disease; Crohn's disease; a; autoimmune disease; allergy; AIDS; us host disease; Alzheimer's disease; arthritis; pain; s disease; Huntington's disease; obesity; diabetes; h; hair loss; asthma; schizophrenia; glomerulonephritis; hematosus; psoriasis; antidiabetic; anorectic; metabolic; neuroprotective; cytostatic; antibacterial; virucide; de; antiarteriosclerotic; hypotensive; cerebroprotective; matory; gynaecological; antiinfectivity; dermatological; ic; haemostatic; immunosuppressive; antiallergic; tic; anticonvulsant; anticseborrhoeic; antiasthmatic; c; anti-HIV; analgesic; nephrotropic; antipsoriatic; PCR;

ns.

7-A2.

2.

12; 2002WO-US022049.

11; 2001US-0268221P.

11; 2001US-0268496P.

11; 2001US-0268646P.

11; 2001US-0268665P.

11; 2001US-0289136P.

11; 2001US-0289310P.

11; 2001US-0269530P.

11; 2001US-0276405P.

11; 2001US-0276399P.

11; 2001US-0276703P.

PR 23-MAR-2001; 2001US-0278199P.
PR 28-MAR-2001; 2001US-0279274P.
PR 30-MAR-2001; 2001US-0280238P.
PR 02-APR-2001; 2001US-0280899P.
PR 08-AUG-2001; 2001US-0310797P.
PR 14-AUG-2001; 2001US-0312284P.
PR 14-SEP-2001; 2001US-0322294P.
PR 14-SEP-2001; 2001US-0322295P.
PR 18-OCT-2001; 2001US-0330293P.
PR 31-OCT-2001; 2001US-0335104P.
PR 31-OCT-2001; 2001US-0335109P.
PR 21-NOV-2001; 2001US-0332127P.
PR 28-NOV-2001; 2001US-0331772P.
XX
XX (CURA-) CURAGEN CORP.

PA Guo X, Fernandes E, Li L, Kekuda R, Liu Y, Leite M, Spyt
XX Ji W, Casman SJ, Boldog FL, Patturajan M, Vernet CAM, Bal
XX Malyankar UM, Tchernev VT, Blalock AD, Gusev VV, Rastelli
PI Mezes PD, Eilerman K, Heyes M, Herrmann JL, Shinkets RA,
PI Pena CEA, Shenoy SG, Taupier RJ, Gerlach V, Gorman L;
XX WPI; 2003-148650/14.

DR Novel NOVX polypeptide useful for identifying an agent that b
XX polypeptide, and for treating cardiomyopathy, atherosclerosis,
XX hypertention, infertility, scleroderma, cirrhosis, and inflam
XX disease.

PS Example 3; Page 415; 566pp; English.

XX The present invention relates to the isolation of novel human
CC polypeptides referred to as NOVX (NOVI-NOV37), variants of the
CC proteins, and the polynucleotide sequences encoding them. The
CC proteins of the invention share homology to various types of p
CC families such as zinc finger-like proteins, enzymes, receptors
CC lipoproteins. The sequences of the invention may be useful in
CC manufacture of a medicament for treating a syndrome associat
CC human disease. For example they can be used to treat inflam
CC disorders, demyelination disease, renal disorders, infections,
CC cardiomyopathy, atherosclerosis, hypertension, stroke, pancre
CC Hippel-Lindau, endometriosis, fertility, scleroderma, cirrho
CC inflammatory bowel disease, Crohn's disease, haemophilia, aut
CC diseases, allergies, graft versus host disease, Alzheimer's di
CC arthritis, Parkinson's disease, Huntington's disease, obesity,
CC acne, hair growth/loss, asthma, schizophrenia, AIDS, pain,
CC glomerulonephritis, lupus erythematosus, and psoriasis. The p
CC sequence represents a PCR primer used in the examples of the i
CC invention. Note: SEQ ID Nos 113-460 are known sequences used i
CC purposes

XX Sequence 22 BP; 4 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 7; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0;

Qy 3 CATCATCCTCTGCATGTCAG 23

Db 1 CCTCATCCTTTTCATGTCAG 21

RESULT 35

ACD20449

ID ACD20449 standard; DNA; 22 BP.

XX AC ACD20449;

XX 26-AUG-2003 (first entry)

DT Human NOVX DNA PCR primer #15.

DE Human; NOVX; inflammatory disorder; demyelination disease; sti

XX Human; NOVX; inflammatory disorder; demyelination disease; sti

XW Human; NOVX; inflammatory disorder; demyelination disease; sti

rd; infection; cardiomyopathy; atherosclerosis; acne;
on; pancreatitis; Von Hippel-Lindau; endometriosis; fertility;
a; cirrhosis; inflammatory bowel disease; Crohn's disease;
a; autoimmune disease; allergy; AIDS;
us host disease; Alzheimer's disease; arthritis; pain;
s disease; Huntington's disease; obesity; diabetes;
h; hair loss; asthma; schizophrenia; glomerulonephritis;
hematocytosis; porosis; antidiabetic; anorectic; metabolic;
neuroprotective; cytostatic; antibacterial; virucide;
de; antiarteriosclerotic; hypotensive; cerebroprotective;
matory; gynaecological; antinfertility; dermatological;
ic; haemostatic; immunosuppressive; antiallergic;
tic; anticonvulsant; antiseborrhoeic; antiasthmatic;
c; anti-HRV; analgesic; nephroretropic; antipsoriatic; PCR;
.

ns.

.7-A2.

12.

12; 2002WO-US022049.

11; 2001US-0268221P.
11; 2001US-0268496P.
11; 2001US-0268646P.
11; 2001US-0268665P.
11; 2001US-0269136P.
11; 2001US-0269310P.
11; 2001US-0269530P.
11; 2001US-0276405P.
11; 2001US-0276399P.
11; 2001US-0276703P.
11; 2001US-0278199P.
11; 2001US-0279274P.
11; 2001US-0280238P.
11; 2001US-0280899P.
11; 2001US-0310797P.
11; 2001US-0312284P.
11; 2001US-0322294P.
11; 2001US-0322295P.
11; 2001US-0330293P.
11; 2001US-0335104P.
11; 2001US-0335109P.
11; 2001US-0332127P.
11; 2001US-0331772P.

IRAGEN CORP.

arnandes E, Li L, Kekuda R, Liu Y, Leite M, Spytek KA;
man SJ, Boldog FI, Patturajan M, Vernet CAM, Ballinger RA;
UM, Tchernev VT, Blalock AD, Gusev VY, Rastelli L;
Ellerman K, Heyes M, Herrmann JL, Shinkets RA, Ioime N;
Shenoy SG, Taupier RJ, Gerlach V, Gorman L;
-148650/14.

(polypeptide useful for identifying an agent that binds to the
le, and for treating cardiomyopathy, atherosclerosis,
on, infertility, scleroderma, cirrhosis, and inflammatory bowel

: Page 415; 566pp; English.

it invention relates to the isolation of novel human
ies referred to as NOVX (NOV1-NOV37), variants of these
and the polynucleotide sequences encoding them. The NOVX
of the invention share homology to various types of protein
such as zinc finger-like proteins, enzymes, receptors, and
ins. The sequences of the invention may be useful in the
re of a medicament for treating a syndrome associated with a
ase. For example they can be used to treat inflammatory

CC disorders, demyelination disease, renal disorders, infections,
CC cardiomyopathy, atherosclerosis, hypertension, stroke, pancrea
CC Hippel-Lindau, endometriosis, fertility, scleroderma, cirrhosi
CC inflammatory bowel disease, Crohn's disease, haemophilia, aut
CC diseases, allergies, graft versus host disease, Alzheimer's di
CC arthritis, Parkinson's disease, Huntington's disease, obesity,
CC acne, hair growth/loss, asthma, schizophrenia, AIDS, pain,
CC glomerulonephritis, lupus erythematosus, and psoriasis. The p
CC sequence represents a PCR primer used in the examples of the i
CC invention. Note: SEQ ID Nos 113-460 are known sequences used f
CC purposes

XX Sequence 22 BP; 4 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 7; Length 22;

Best Local Similarity 81.0%; Pred. No. 1.1e+04;

Matches 17; Conservative 0; Mismatches 4; Indels 0;

Qy 3 CATCATCCTCTGTCATGTCAG 23

Db 1 CCTCATCCTTTTCATGTCAG 21

RESULT 36

AC100102

ID AC100102 standard; DNA; 25 BP.

XX AC AC100102;

XX AC AC100102;

DT 13-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 93.

XX EST; ss; probe; expressed sequence tag; microarray; gene expre
Genetic variation; biallelic marker; polymorphism; human;
cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

PD 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridiza
Southern, Northern or dot-blot hybridization to identify or de
sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 93; 9pp; English.

XX The invention discloses a microarray comprising a plurality of
acid probes including one of 2,018,500 fully defined sequences
perfect match, perfect mismatch, antisense match or antisense
Also disclosed is a method of gene expression analysis. The ar
in monitoring gene expression levels by hybridisation to a DN
in analysis of genetic variation or in hybridisation of tag-la
compounds. The nucleic acid probes are specifically designed f
of at least one target sequence. The method of analysis compri
hybridising at least one or more nucleic acids to at least two
nucleic acid probes and detecting the hybridisation. The nucle
probes are attached to a solid support. The analysis comprises
gene expression levels, identifying biallelic markers or polyn
or family members of a gene and a cross-species comparison. Ea
nucleic acids further comprises a tag sequence. The array of r

useful in in situ hybridisation, in Southern, Northern or dot-probe hybridisation to identify or detect the sequence or specific regions of any gene, in mapping the 5' termini of mRNA molecules or subclones containing segments of DNA that have been previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic form at seqdata.uspto.gov/sequence.html

25 BP; 4 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 8; Length 25;

Best Local Similarity 81.0%; Pred. No. 1.1e+04;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

AGCATCCTCTCTGCATGTC 21

||||| ||||| ||||| ||||| |||||

AGCATCCGCTCTCTGCAGGTC 24

standard; DNA; 25 BP.

33 (first entry)

array DNA oligonucleotide SEQ ID NO 94.

probe: expressed sequence tag; microarray; gene expression; hybridization; biallelic marker; polymorphism; human; comparison.

ns.

10-A1.

33.

12; 2002US-00098263.

1; 2001US-0276759P.

MYMETRIX INC.

IP;

567953/53.

of nucleic acid probes, useful for in situ hybridization, in Northern or dot-blot hybridization to identify or detect the or specific mutations of any gene.

SEQ ID NO 94; 9pp; English.

ion discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its subclones, perfect mismatch, antisense match or antisense mismatch. The array is a method of gene expression analysis. The array is used for gene expression levels by hybridization to a DNA library, or of genetic variation or in hybridization of tag-labelled nucleic acid probes are specifically designed for analysis of one target sequence. The method of analysis comprises hybridization of at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridization. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring expression levels, identifying biallelic markers or polymorphisms, members of a gene and a cross-species comparison. Each of the arrays further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridization, in Southern, Northern or dot-probe hybridization to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molecules or primer extensions or in screening cDNA or genomic libraries or for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic form at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 5 A; 9 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 8; Length 25;

Best Local Similarity 81.0%; Pred. No. 1.1e+04;

Matches 17; Conservative 0; Mismatches 4; Indels 0

QY 1 AGCATCCTCTCTGCATGTC 21

||||| ||||| ||||| ||||| |||||

Db 4 AGCATCCGCTCTCTGCAGGTC 24

RESULT 38

AAV46380/c

ID AAV46380 standard; DNA; 30 BP.

XX

AC AAV46380;

XX

DT 20-NOV-1998 (first entry)

XX

DE PCR primer of the invention.

XX

KW Mouse; CXC chemokine receptor; pre-B cell line DW34;

KW CXC chemokine pre-B cell stimulatory factor PBSF/SDF-1; HIV i;

KW screening; inhibitor; AIDS; PCR primer; ss.

XX

OS Synthetic.

XX

PN WO9835035-A1.

XX

PD 13-AUG-1998.

XX

PF 07-FEB-1997; 97WO-JP000299.

XX

PR 07-FEB-1997; 97WO-JP000299.

XX

PA (SHIO) SHIONOGI & CO LTD.

XX

PI Kishimoto T, Nagasawa T, Tachibana K, Iizasa H, Yoshida N,

PI Nakajima T, Yoshie O;

XX

DR WPI; 1998-447232/38.

XX

PT Mouse CXC chemokine receptor binding to PBSF/SDF-1 pre-B cell

PT factor - is useful for screening of potential HIV infection at

PT inhibitors.

XX

PS Example 5; Page 52; 76pp; Japanese.

XX

CC PCR primers AAV46380-81 are used in the course of the invention

CC specification describes a murine CXC chemokine receptor which

CC the mouse CXC chemokine pre-B cell stimulatory factor PBSF/SDF-1

CC nucleic acid is isolated from mouse pre-B cell line DW34. The

CC and cells expressing it can be used in the study and mapping of

CC mechanism of HIV infection and in screening of potential inhibitors

CC HIV infection and the development of AIDS

XX Sequence 30 BP; 6 A; 7 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 2; Length 30;

Best Local Similarity 81.0%; Pred. No. 1.1e+04;

Matches 17; Conservative 0; Mismatches 4; Indels 0;

QY 6 CATCCTCTCTGCATGTCAGGTC 26

||||| ||||| ||||| ||||| |||||

Db 27 CATCCCTCTCTGCATGTAACGTC 7

standard; DNA; 34 BP.

03 (first entry)

r #6 used for generating chimeric Edg5 receptors.
g; receptor; PCR; primer; ss.
ens.

503-A1.

03.

02; 2002WO-US022346.

01; 2001US-00904099.

ERE TEK.

Munning JN, Spencer JV;
-221718/21.

tic Edg receptor, useful in high-throughput screening assays,
extracellular and transmembrane domains of a first Edg
and a chimeric intracellular domain of a second Edg receptor.

Page 38; 71pp; English.

it invention relates to Edg receptors (ABP59277-ABP59290). The
ors, are useful in a high-throughput screening assay to
compounds that bind to or modulate the activity of the
e, in calcium mobilisation assays, binding assays, detection of
tion, or in reporter gene techniques. The present sequence is a
; which was used for generating chimeric Edg1 receptors

14 BP; 7 A; 9 C; 10 G; 8 T; 0 U; 0 Other;
milarity 52.1%; Score 14.6; DB 7; Length 34;
Conservative 0; Pred. No. 1.2e+04; Mismatches 4; Indels 0;
ATCTCTGCGTGGTCAAGTC 26
ATCTACTGCGTGGTCAAGTC 14

standard; DNA; 34 BP.

3 (first entry)

#5 used for generating chimeric Edg5 receptors.
i; receptor; PCR; primer; ss.
ns.

03-A1.

3.

2; 2002WO-US022346.

XX 11-JUL-2001; 2001US-00904099.
XX (CERE-) CERETEK.
XX Shankar G, Munning JN, Spencer JV;
XX WPI; 2003-221718/21.
XX New chimeric Edg receptor, useful in high-throughput screenin
XX comprises extracellular and transmembrane domains of a first
XX receptor, and a chimeric intracellular domain of a second Edg
XX Example; Page 38; 71pp; English.
XX The present invention relates to Edg receptors (ABP59277-ABP5
XX Edg receptors, are useful in a high-throughput screening assa
XX identify compounds that bind to or modulate the activity of t
XX polypeptide, in calcium mobilisation assays, binding assays,
XX CAMP formation, or in reporter gene techniques. The present s
XX PCR primer, which was used for generating chimeric Edg1 recep
XX Sequence 34 BP; 8 A; 10 C; 9 G; 7 T; 0 U; 0 Other;
XX Query Match 52.1%; Score 14.6; DB 7; Length 34;
XX Best Local Similarity 81.0%; Pred. No. 1.2e+04;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0
Qy 6 CATCTCTGCGTGGTCAAGTC 26
Db 1 CATCTACTGCGTGGTCAAGTC 21

Search completed: April 12, 2004, 16:42:48
Job time : 208.077 secs

GenCore version 5.1.6
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ncleic search, using sw model

April 12, 2004, 15:31:02 ; Search time 478.769 Seconds
(without alignments)
2534.843 Million cell updates/sec

US-10-090-326-23

28

1 agcatatccctctgcaggtcaggtcat 28

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

3470272 seqs, 21671516995 residues

: hits satisfying chosen parameters: 1685580

length: 0
length: 60

! Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.man.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Descrip
1	20	71.4	20	6	AX001634	AX00163
2	20	71.4	20	6	AX002137	AX00213
3	20	71.4	20	6	AX816396	AX81639
4	20	71.4	20	6	BD195919	BD19591
5	18	64.3	30	6	A98653	A98653
6	17.2	61.4	40	6	AX538397	AX53839
7	17	60.7	40	6	AX538396	AX53839
8	16	57.1	29	6	A75717	A75717
9	16	57.1	29	6	E06837	E06837
10	16	57.1	42	6	AX328821	AX32882
11	16	57.1	42	6	BD132386	BD13238
12	15.6	55.7	30	6	AR069517	AR06951
13	15.6	55.7	30	6	BD195684	BD19568
14	15.2	54.3	33	6	BD266770	BD26677
15	15.2	54.3	33	6	AX395703	AX39570
16	15.2	54.3	35	6	A11296	A11296
17	15.2	54.3	38	6	A11037	A11037
18	15.2	54.3	41	6	A11036	A11036
19	15.2	54.3	41	6	A11295	A11295
20	15.2	54.3	56	6	E15475	E15475
21	15.2	54.3	58	6	AX327977	AX32797
22	15	53.6	44	6	AX254656	AX25465
23	14.8	52.9	31	6	BD002886	BD00288
24	14.8	52.9	40	6	A83618	A83618
25	14.8	52.9	46	6	AX598134	AX59813
26	14.8	52.9	50	6	AR148167	AR14816
27	14.8	52.9	51	6	AX157925	AX15792
28	14.8	52.9	60	6	BD227015	BD22701
29	14.6	52.1	22	6	AX769362	AX76936
30	14.6	52.1	22	6	AX769365	AX76936
31	14.6	52.1	40	6	AR148762	AR14876
32	14.6	52.1	45	6	AX234368	AX23436
33	14.6	52.1	46	6	AX234359	AX23435
34	14.6	52.1	51	6	AX165131	AX16513
35	14.4	51.4	26	6	AR028646	AR02864
36	14.4	51.4	26	6	AR053739	AR05373
37	14.4	51.4	26	6	AR146239	AR14623
38	14.4	51.4	26	6	AR178189	AR17818
39	14.4	51.4	26	6	I73318	I73318
40	14.4	51.4	26	6	AR214471	AR21447
41	14.4	51.4	26	6	AR274829	AR27482
42	14.4	51.4	31	6	AX248051	AX24805
43	14.4	51.4	42	6	I43112	I43112
44	14.4	51.4	47	6	A87110	A87110
45	14.4	51.4	47	6	AR206364	AR20636
46	14.4	51.4	47	6	BD069870	BD06987
47	14.4	51.4	51	6	AR166270	AR16627
48	14.4	51.4	53	6	AR147183	AR14718
49	14.4	51.4	53	6	BD083543	BD08354
50	14.4	51.4	54	6	AX203052	AX20305
51	14.4	51.4	55	6	AR147184	AR14718
52	14.4	51.4	55	6	AX023568	AX02356
53	14.4	51.4	55	6	BD083544	BD08354
54	14.2	50.7	22	6	BD016506	BD01650
55	14.2	50.7	24	6	BD131527	BD13152
56	14.2	50.7	29	6	AR126584	AR12658
57	14.2	50.7	30	6	BD174399	BD17439
58	14.2	50.7	41	6	AX519250	AX51925
59	14.2	50.7	41	6	AX519259	AX51925
60	14.2	50.7	44	6	AX128565	AX12856
61	14.2	50.7	45	6	BD247648	BD24764
62	14.2	50.7	45	6	AR345117	AR34511
63	14.2	50.7	51	6	A45055	A45055
64	14.2	50.7	51	6	AR029671	AR02967
65	14.2	50.7	51	6	AX159509	AX15950

50.7	51	6	AX204361	Sequence	C 139	13.6	48.6	25	6	AX615701	AX61570
50.7	57	6	A45746	Sequence 3	C 140	13.6	48.6	25	6	AX615702	AX61570
50.7	57	6	AR372860	Sequence	C 141	13.6	48.6	30	6	AX793680	AX79368
50.7	58	12	AY199433	Arabidops	142	13.6	48.6	34	6	AR085288	AR08528
50.0	25	6	AX224545	Sequence	143	13.6	48.6	34	6	I17719	I17719
50.0	27	6	AX662247	Sequence	144	13.6	48.6	34	6	I28967	I28967
50.0	29	6	AX099620	Sequence	145	13.6	48.6	34	6	I38631	I38631
50.0	29	6	BD063996	Secreted	146	13.6	48.6	34	6	I38889	I38889
50.0	30	6	E27900	Yeast with	147	13.6	48.6	34	6	I68974	I68974
50.0	30	6	BD016617	Genes and	148	13.6	48.6	36	6	I68976	I68976
50.0	31	6	AX538109	Sequence	149	13.6	48.6	36	6	AR253572	AR25357
50.0	32	6	BD022557	Multi-fun	150	13.6	48.6	36	6	AR253574	AR25357
50.0	35	6	AR166262	Sequence	151	13.6	48.6	36	6	AX696627	AX69662
50.0	38	6	AR063464	Sequence	152	13.6	48.6	36	6	AX696629	AX69662
50.0	41	6	AX515904	Sequence	153	13.6	48.6	40	6	BD188745	BD18874
50.0	41	6	AX515904	Sequence	154	13.6	48.6	40	6	BD188745	BD18874
50.0	45	12	D64063	Synthetic C	155	13.6	48.6	42	6	BD246948	BD24694
50.0	47	6	AX194785	Sequence	156	13.6	48.6	44	6	AR096941	AR09694
50.0	50	6	AX418552	Sequence	157	13.6	48.6	45	6	AX695192	AX69519
50.0	51	6	AX026023	Sequence	158	13.6	48.6	45	6	A45567	A45567
50.0	51	6	AX161873	Sequence	159	13.6	48.6	49	6	A47605	A47605
50.0	51	6	AX161874	Sequence	160	13.6	48.6	49	6	AX019331	AX01933
50.0	51	6	AX165491	Sequence	161	13.6	48.6	49	6	A98797	A98797
50.0	60	6	E27896	Yeast with	162	13.6	48.6	50	6	AR242325	AR24232
50.0	60	6	E41219	Specific cu	163	13.6	48.6	51	6	AX165610	AX16561
49.3	20	6	AR231034	Sequence	164	13.6	48.6	57	6	BD138415	BD13841
49.3	21	6	AR028691	Sequence	165	13.6	48.6	60	10	AF432391	AF4323
49.3	21	6	AR086502	Sequence	166	13.6	48.6	25	6	E05089	E05089
49.3	27	6	AR143805	Sequence	167	13.4	47.9	26	6	AR065340	AR06534
49.3	30	6	AX792455	Sequence	168	13.4	47.9	27	6	AR365085	AR36508
49.3	32	6	BD261368	Plants, S	169	13.4	47.9	27	6	AR365086	AR36508
49.3	32	6	AR184304	Sequence	170	13.4	47.9	29	6	BD191423	BD19142
49.3	32	6	AR431246	Sequence	171	13.4	47.9	30	6	AX792518	AX79251
49.3	32	6	BD132769	Fatty aci	172	13.4	47.9	33	6	AR146987	AR14698
49.3	34	6	BD244058	Determina	173	13.4	47.9	41	6	AR109079	AR10907
49.3	42	6	A47188	Sequence 1	174	13.4	47.9	41	6	AR200734	AR20073
49.3	42	6	I79600	Sequence 1	175	13.4	47.9	41	6	AX515868	AX51586
49.3	43	6	I43892	Sequence 20	176	13.4	47.9	41	6	AX521125	AX52112
49.3	46	6	BD244069	Determina	177	13.4	47.9	41	6	AX521140	AX52114
49.3	50	6	AX204297	Sequence	178	13.4	47.9	43	6	BD232717	BD23271
49.3	51	6	AR343496	Sequence	179	13.4	47.9	45	6	AX023259	AX02325
49.3	52	6	AR021007	Sequence	180	13.4	47.9	45	6	A48442	A48442
49.3	52	6	AR043422	Sequence	181	13.4	47.9	46	8	S57736	S57736
49.3	52	6	AR043462	Sequence	182	13.4	47.9	51	6	AX115441	AX11544
49.3	52	6	AR062337	Sequence	183	13.4	47.9	55	6	AR428091	AR42809
49.3	52	6	AR062337	Sequence	184	13.4	47.9	60	6	AX454000	AX45400
49.3	52	6	AR183796	Sequence	185	13.4	47.9	60	6	AX454001	AX45400
49.3	52	6	AR183836	Sequence	186	13.4	47.9	20	6	AR316159	AR31615
49.3	52	6	AR368179	Sequence	187	13.4	47.9	21	6	AR272208	AR27220
49.3	54	6	BD71048	Method an	188	13.2	47.1	21	6	AX097296	AX09729
49.3	54	6	AR258454	Sequence	189	13.2	47.1	24	6	AR167458	AR16745
49.3	59	6	AX011479	Sequence	191	13.2	47.1	24	6	I14554	I14554
49.3	59	6	BD225770	Screening	193	13.2	47.1	24	6	AX05673	AX05673
49.3	60	3	TG28SRNAB	Tetrahicho	195	13.2	47.1	24	6	AX110200	AX11020
49.3	60	6	AX453999	Sequence	196	13.2	47.1	25	6	BD245828	BD24582
48.6	20	6	AX505100	Sequence	197	13.2	47.1	25	6	AR181350	AR18135
48.6	21	6	AR242920	Sequence	198	13.2	47.1	25	6	AX615695	AX61569
48.6	21	6	AR363537	Sequence	199	13.2	47.1	25	6	AX615696	AX61569
48.6	21	6	AX384972	Sequence	200	13.2	47.1	26	6	AR090772	AR09077
48.6	23	6	AR102043	Sequence	201	13.2	47.1	26	6	AR197807	AR19780
48.6	23	6	AR134826	Sequence	202	13.2	47.1	26	6	AR259961	AR25996
48.6	23	6	AX708837	Sequence	203	13.2	47.1	29	6	AR429703	AR42970
48.6	23	6	AX708851	Sequence	204	13.2	47.1	30	6	AR142231	AR14223
48.6	24	6	AX020807	Sequence	205	13.2	47.1	30	6	I34492	I34492
48.6	24	6	AX652073	Sequence	206	13.2	47.1	30	6	I57327	I57327
48.6	25	6	E40339	DNA marker	207	13.2	47.1	30	6	I73205	I73205
48.6	25	6	AX615697	Sequence	208	13.2	47.1	30	6	AX449613	AX44961
48.6	25	6	AX615698	Sequence	209	13.2	47.1	30	6	AX791495	AX79149
48.6	25	6	AX615699	Sequence	210	13.2	47.1	30	6	AX792499	AX79249
48.6	25	6	AX615700	Sequence	211	13.2	47.1	30	6	AX793843	AX79384

45.7	45.7	38	6	BD057965	BD057965 Nucleic a	C 431	12.6	45.0	25	6	E17259	E17259 F
45.7	45.7	41	6	AX517120	AX517120 Sequence	432	12.6	45.0	25	6	E22978	E22978 V
45.7	45.7	41	6	AX519649	AX519649 Sequence	C 433	12.6	45.0	25	6	E22979	E22979 V
45.7	45.7	42	6	A11038	A11038 Nucleotide	434	12.6	45.0	25	6	AR219925	AR219925
45.7	45.7	42	6	A11039	A11039 Nucleotide	C 435	12.6	45.0	25	6	AR219926	AR219926
45.7	45.7	42	6	A11299	A11299 Nucleotide	C 436	12.6	45.0	25	6	AX609254	AX609254
45.7	45.7	42	6	A11300	A11300 Nucleotide	C 437	12.6	45.0	25	6	AX609397	AX609397
45.7	45.7	43	6	AR061569	AR061569 Sequence	C 438	12.6	45.0	25	6	AX609713	AX609713
45.7	45.7	43	6	AR108468	AR108468 Sequence	C 439	12.6	45.0	25	6	AX615703	AX615703
45.7	45.7	43	6	I16425	I16425 Sequence 25	440	12.6	45.0	27	6	AR126153	AR126153
45.7	45.7	43	6	I66911	I66911 Sequence 25	C 441	12.6	45.0	27	6	AX813718	AX813718
45.7	45.7	43	6	I85005	I85005 Sequence 25	442	12.6	45.0	28	6	AX813719	AX813719
45.7	45.7	43	6	AR263429	AR263429 Sequence	443	12.6	45.0	30	6	AX468557	AX468557
45.7	45.7	44	6	A92629	A92629 Sequence 1	444	12.6	45.0	30	6	AX521574	AX521574
45.7	45.7	45	6	AR152959	AR152959 Sequence	445	12.6	45.0	30	6	AX791712	AX791712
45.7	45.7	45	6	BD264361	BD264361 Methods a	446	12.6	45.0	30	6	AX792861	AX792861
45.7	45.7	45	6	AR199548	AR199548 Sequence	447	12.6	45.0	30	6	AX793820	AX793820
45.7	45.7	45	6	AR374700	AR374700 Sequence	448	12.6	45.0	30	9	HUMPLT22	U37829 H
45.7	45.7	45	6	AR409335	AR409335 Sequence	C 449	12.6	45.0	31	6	AR195945	AR195945
45.7	45.7	45	6	AR429076	AR429076 Sequence	C 450	12.6	45.0	31	6	AX248399	AX248399
45.7	45.7	45	6	AX239597	AX239597 Sequence	C 451	12.6	45.0	31	6	AX249041	AX249041
45.7	45.7	45	6	BD022692	BD022692 Method fo	452	12.6	45.0	32	6	AR102441	AR102441
45.7	45.7	45	6	BD056462	BD056462 Novel low	453	12.6	45.0	32	6	AR219355	AR219355
45.7	45.7	45	6	BD140557	BD140557 Polypepti	454	12.6	45.0	32	6	BD138423	BD138423
45.7	45.7	46	6	AX800151	AX800151 Sequence	C 455	12.6	45.0	33	6	A84476	A84476 S
45.7	45.7	47	6	AR290446	AR290446 Sequence	C 456	12.6	45.0	33	6	AR279934	AR279934
45.7	45.7	47	6	BD080451	BD080451 Methods f	457	12.6	45.0	33	6	AX306751	AX306751
45.7	45.7	51	6	AR077801	AR077801 Sequence	C 458	12.6	45.0	33	6	AX306752	AX306752
45.7	45.7	51	6	BD227170	BD227170 Protease	C 459	12.6	45.0	33	6	AX427375	AX427375
45.7	45.7	51	6	AR368746	AR368746 Sequence	C 460	12.6	45.0	33	6	BD082556	BD082556
45.7	45.7	51	6	AX158409	AX158409 Sequence	C 461	12.6	45.0	34	6	AX548220	AX548220
45.7	45.7	51	6	AX158411	AX158411 Sequence	462	12.6	45.0	35	6	AX794614	AX794614
45.7	45.7	51	6	AX158412	AX158412 Sequence	463	12.6	45.0	35	6	AX794663	AX794663
45.7	45.7	51	6	AX162007	AX162007 Sequence	464	12.6	45.0	36	6	A51534	A51534 S
45.7	45.7	51	6	AX204357	AX204357 Sequence	465	12.6	45.0	36	6	A51562	A51562 S
45.7	45.7	51	9	HSCDICC	X79310 H.sapiens C	466	12.6	45.0	36	6	A87816	A87816 S
45.7	45.7	52	14	ADYLTR	M17114 Avian egg d	467	12.6	45.0	36	6	A91148	A91148 S
45.7	45.7	54	6	I51658	I51658 Sequence 5	468	12.6	45.0	36	6	AR084288	AR084288
45.7	45.7	54	6	AX471970	AX471970 Sequence	469	12.6	45.0	36	6	AR119408	AR119408
45.7	45.7	59	6	AR7307	AR7307 Sequence 32	470	12.6	45.0	36	6	AR173499	AR173499
45.7	45.7	59	6	BD057385	BD057385 Protein c	471	12.6	45.0	36	6	I95566	I95566 S
45.7	45.7	60	6	AR172702	AR172702 Sequence	C 472	12.6	45.0	36	6	AX026033	AX026033
45.7	45.7	60	6	AR178646	AR178646 Sequence	C 473	12.6	45.0	36	6	AX026033	AX026033
45.7	45.7	60	6	BD231090	BD231090 Shuffling	474	12.6	45.0	36	6	BD064628	BD064628
45.7	45.7	60	6	AR181217	AR181217 Sequence	475	12.6	45.0	36	6	BD067141	BD067141
45.7	45.7	60	6	AR199898	AR199898 Sequence	476	12.6	45.0	36	6	BD135011	BD135011
45.7	45.7	60	6	AR231846	AR231846 Sequence	C 477	12.6	45.0	37	6	AR110221	AR110221
45.7	45.7	60	6	AR343321	AR343321 Sequence	C 478	12.6	45.0	37	6	AR169980	AR169980
45.7	45.7	60	6	AR349639	AR349639 Sequence	C 479	12.6	45.0	37	6	AR171789	AR171789
45.7	45.7	60	6	AR391110	AR391110 Sequence	C 480	12.6	45.0	37	6	AR201269	AR201269
45.7	45.7	60	6	AR431553	AR431553 Sequence	C 481	12.6	45.0	37	6	AR264126	AR264126
45.7	45.7	60	6	AX280278	AX280278 Sequence	C 482	12.6	45.0	37	6	AR264126	AR264126
45.7	45.7	60	6	AX280280	AX280280 Sequence	C 483	12.6	45.0	37	6	AX617004	AX617004
45.7	45.7	60	6	BD062835	BD062835 Methods a	C 484	12.6	45.0	37	6	BD009014	BD009014
45.0	45.0	19	6	AX480658	AX480658 Sequence	C 485	12.6	45.0	37	6	BD189483	BD189483
45.0	45.0	20	6	AR118940	AR118940 Sequence	C 486	12.6	45.0	39	6	AR002625	AR002625
45.0	45.0	20	6	I19480	I19480 Sequence 12	C 487	12.6	45.0	39	6	AR002625	AR002625
45.0	45.0	20	6	AX254738	AX254738 Sequence	C 488	12.6	45.0	40	6	AR205021	AR205021
45.0	45.0	20	6	AX255088	AX255088 Sequence	C 489	12.6	45.0	40	6	AX538569	AX538569
45.0	45.0	21	6	BD266110	BD266110 Universal	C 490	12.6	45.0	41	6	AR264225	AR264225
45.0	45.0	21	6	BD016749	BD016749 Identific	491	12.6	45.0	41	6	AX514034	AX514034
45.0	45.0	22	6	A47330	A47330 Sequence 5	492	12.6	45.0	41	6	AX516099	AX516099
45.0	45.0	22	6	AR097970	AR097970 Sequence	493	12.6	45.0	41	6	AX517505	AX517505
45.0	45.0	22	6	AR145812	AR145812 Sequence	494	12.6	45.0	41	6	AX518475	AX518475
45.0	45.0	22	6	EO8175	EO8175 Reverse pri	495	12.6	45.0	41	6	AX520503	AX520503
45.0	45.0	22	6	AR283937	AR283937 Sequence	496	12.6	45.0	41	6	AX580276	AX580276
45.0	45.0	22	6	AX356176	AX356176 Sequence	497	12.6	45.0	41	6	AX786441	AX786441
45.0	45.0	22	6	AX528227	AX528227 Sequence	C 498	12.6	45.0	44	6	E43912	E43912 N
45.0	45.0	22	6	BD144849	BD144849 A method	C 499	12.6	45.0	45	6	AR099099	AR099099
45.0	45.0	22	6	BD182884	BD182884 PCA3dd3	C 500	12.6	45.0	45	6	AR199538	AR199538
45.0	45.0	24	6	AR098842	AR098842 Sequence	C 501	12.6	45.0	45	6	AR174690	AR174690
45.0	45.0	25	6	E17258	E17258 Primer. 7/1	C 502	12.6	45.0	45	6	AR409325	AR409325
45.0	45.0	25	6			503	12.6	45.0	45	6	AX224742	AX224742

45.0	45	6	AX239587	Sequence	577	12.4	44.3	31	6	AR259307	AX259307
45.0	45	6	BD056452	Novel low	578	12.4	44.3	31	6	AX172826	AX172826
45.0	46	6	AR277862	Sequence	C 579	12.4	44.3	32	6	AR017664	AR017664
45.0	47	6	AR077831	Sequence	C 580	12.4	44.3	32	6	AR030309	AR030309
45.0	47	6	AR288348	Sequence	C 581	12.4	44.3	32	6	AR042852	AR042852
45.0	48	9	HSTCELL20	Sequence	C 582	12.4	44.3	32	6	AR054846	AR054846
45.0	48	9	S90755	H sapiens r	C 583	12.4	44.3	32	6	AR058793	AR058793
45.0	48	9	S90756	V delta 1,	C 584	12.4	44.3	32	6	AR063519	AR063519
45.0	50	6	BD273138	S90756 V delta 1,	C 585	12.4	44.3	32	6	AR064785	AR064785
45.0	51	6	A45564	BD273138 Oral immu	C 586	12.4	44.3	32	6	AR066111	AR066111
45.0	51	6	A45565	A45564 Sequence 2	C 587	12.4	44.3	32	6	AR081343	AR081343
45.0	51	6	AR019338	A45565 Sequence 3	C 588	12.4	44.3	32	6	AR092167	AR092167
45.0	51	6	AR019332	Sequence	C 589	12.4	44.3	32	6	AR094841	AR094841
45.0	51	6	AR069999	Sequence	C 590	12.4	44.3	32	6	AR118158	AR118158
45.0	51	6	AR151083	Sequence	C 591	12.4	44.3	32	6	AR122782	AR122782
45.0	51	6	I25437	AR151083 Sequence	C 592	12.4	44.3	32	6	AR125757	AR125757
45.0	51	6	I60623	I25437 Sequence 3	C 593	12.4	44.3	32	6	AR140767	AR140767
45.0	51	6	AR235874	I60623 Sequence 3	C 594	12.4	44.3	32	6	AR151286	AR151286
45.0	51	6	AX159338	AR235874 Sequence	C 595	12.4	44.3	32	6	AR165500	AR165500
45.0	51	6	AX164856	AX159338 Sequence	C 596	12.4	44.3	32	6	I40674	I40674
45.0	51	6	AX165333	AX164856 Sequence	C 597	12.4	44.3	32	6	I42322	I42322
45.0	51	6	AX189855	AX165333 Sequence	C 598	12.4	44.3	32	6	I47169	I47169
45.0	51	6	AX203981	AX189855 Sequence	C 599	12.4	44.3	32	6	I73549	I73549
45.0	51	6	AX203981	AX203981 Sequence	C 600	12.4	44.3	32	6	I93446	I93446
45.0	51	6	AX204433	AX204433 Sequence	C 601	12.4	44.3	32	6	I95073	I95073
45.0	51	6	BD073552	BD073552 High expr	C 602	12.4	44.3	32	6	AR193198	AR193198
45.0	51	10	MUSMHCML	KO0986 Mouse adult	C 603	12.4	44.3	32	6	AR221664	AR221664
45.0	52	6	AR065169	AR065169 Sequence	C 604	12.4	44.3	32	6	AR304702	AR304702
45.0	54	6	I13039	I13039 Sequence 16	C 605	12.4	44.3	32	6	AR337318	AR337318
45.0	54	6	I13040	I13040 Sequence 17	C 606	12.4	44.3	32	6	AR360441	AR360441
45.0	54	6	AX056665	AX056665 Sequence	C 607	12.4	44.3	32	6	AR372166	AR372166
45.0	54	6	AX912408	AX912408 Sequence	C 608	12.4	44.3	32	6	AX027871	AX027871
45.0	54	6	BD047941	BD047941 Sequence	C 609	12.4	44.3	32	6	AX708231	AX708231
45.0	55	6	E15763	E15763 PCR primer	C 610	12.4	44.3	32	6	BD022895	BD022895
45.0	55	6	E26731	E26731 Vertebrate	C 611	12.4	44.3	32	6	BD130678	BD130678
45.0	57	6	AX612611	AX612611 Sequence	C 612	12.4	44.3	33	6	AR054771	AR054771
45.0	57	6	AX612612	AX612612 Sequence	C 613	12.4	44.3	33	6	AR066036	AR066036
45.0	60	6	AX521516	AX521516 Sequence	C 614	12.4	44.3	33	6	I08861	I08861
44.3	17	6	AX730994	AX730994 Sequence	C 615	12.4	44.3	33	6	AX172827	AX172827
44.3	20	6	BD136731	AX757880 Sequence	C 616	12.4	44.3	33	6	AX172828	AX172828
44.3	22	6	AR136528	BD136731 Best/s ma	C 617	12.4	44.3	34	6	AR174599	AR174599
44.3	22	6	AR136593	AR136528 Sequence	C 618	12.4	44.3	34	6	BD248992	BD248992
44.3	23	6	AX675167	AR136593 Sequence	C 619	12.4	44.3	34	6	AR374091	AR374091
44.3	23	6	BD123410	AX675167 Sequence	C 620	12.4	44.3	35	6	A71940	A71940
44.3	24	6	AX535397	BD123410 SREP-2 g	C 621	12.4	44.3	35	6	AR013969	AR013969
44.3	24	6	BD084848	AX535397 Sequence	C 622	12.4	44.3	35	6	AR147128	AR147128
44.3	25	6	AX532762	BD084848 Modified	C 623	12.4	44.3	35	6	E06663	E06663
44.3	25	6	AX532763	AX532762 Sequence	C 624	12.4	44.3	35	6	I25604	I25604
44.3	25	6	AX609296	AX532763 Sequence	C 625	12.4	44.3	35	6	AR236289	AR236289
44.3	25	6	AX674949	AX609296 Sequence	C 626	12.4	44.3	35	6	BD009816	BD009816
44.3	27	6	AX172822	AX674949 Sequence	C 627	12.4	44.3	35	6	BD251194	BD251194
44.3	28	6	AX049558	AX172822 Sequence	C 628	12.4	44.3	36	6	AX172829	AX172829
44.3	29	6	AR014455	AX049558 Sequence	C 629	12.4	44.3	36	6	AR070957	AR070957
44.3	29	6	AX172824	AR014455 Sequence	C 630	12.4	44.3	38	6	AX219312	AX219312
44.3	30	6	AR011860	AX172824 Sequence	C 631	12.4	44.3	39	6	AR002612	AR002612
44.3	30	6	AR129097	AR011860 Sequence	C 632	12.4	44.3	39	6	AR099662	AR099662
44.3	30	6	BD243448	AR129097 Sequence	C 633	12.4	44.3	40	6	AR006865	AR006865
44.3	30	6	I77183	BD243448 Nucleic a	C 634	12.4	44.3	40	6	AR081345	AR081345
44.3	30	6	AX172825	I77183 Sequence 55	C 635	12.4	44.3	40	6	I42324	I42324
44.3	30	6	AX280502	AX172825 Sequence	C 636	12.4	44.3	40	6	I73551	I73551
44.3	30	6	AX361077	AX280502 Sequence	C 637	12.4	44.3	40	6	I74805	I74805
44.3	30	6	AX377765	AX361077 Sequence	C 638	12.4	44.3	40	6	AX538355	AX538355
44.3	30	6	AX791897	AX377765 Sequence	C 639	12.4	44.3	40	6	AX538495	AX538495
44.3	30	6	AX792486	AX791897 Sequence	C 640	12.4	44.3	40	6	AX538500	AX538500
44.3	30	6	AX792508	AX792486 Sequence	C 641	12.4	44.3	40	6	AX680278	AX680278
44.3	30	6	AX793272	AX792508 Sequence	C 642	12.4	44.3	40	6	AX708233	AX708233
44.3	30	6	AX793282	AX793272 Sequence	C 643	12.4	44.3	40	6	AX786443	AX786443
44.3	31	6	AR076337	AX793282 Sequence	C 644	12.4	44.3	40	6	BD086562	BD086562
44.3	31	6	AR090118	AR076337 Sequence	C 645	12.4	44.3	41	6	AS1529	AS1529
44.3	31	6	BD234280	AR090118 Sequence	C 646	12.4	44.3	41	6	AS1557	AS1557
44.3	31	6	I72704	BD234280 Antisense	C 647	12.4	44.3	41	6		
44.3	31	6	AR197153	I72704 Sequence 71	C 648	12.4	44.3	41	6		
44.3	31	6		AR197153 Sequence	C 649	12.4	44.3	41	6		

44.3	41	5	A87822	A87822 Sequence 18	723	12.4	44.3	60	5	A8226370	AR22637
44.3	41	6	A91154	A91154 Sequence 18	C 724	12.4	44.3	60	9	A450279	AF45027
44.3	41	6	AR084283	AR084283 Sequence	725	12.2	43.6	17	6	BD259541	BD25954
44.3	41	6	AR119414	AR119414 Sequence	C 726	12.2	43.6	17	6	AX615418	AX61541
44.3	41	6	AR173505	AR173505 Sequence	C 727	12.2	43.6	17	6	AX615419	AX61541
44.3	41	6	I95561	I95561 Sequence 15	728	12.2	43.6	17	6	AX648762	AX64876
44.3	41	6	AX172830	AX172830 Sequence	C 729	12.2	43.6	17	6	AX724452	AX72445
44.3	41	6	AX327077	AX327077 Sequence	C 730	12.2	43.6	17	6	AX728429	AX72842
44.3	41	6	AX514396	AX514396 Sequence	C 731	12.2	43.6	17	6	AX736206	AX73620
44.3	41	6	AX516182	AX516182 Sequence	732	12.2	43.6	18	6	AR119919	AR11991
44.3	41	6	AX521242	AX521242 Sequence	733	12.2	43.6	18	6	AR337656	AR33765
44.3	41	6	BD064634	BD064634 Live reco	734	12.2	43.6	18	6	AX137278	AX13727
44.3	41	6	BD067147	BD067147 Avian rec	735	12.2	43.6	18	6	BD013853	BD01385
44.3	43	6	A83396	A83396 Sequence 1	736	12.2	43.6	19	6	AX412047	AX41204
44.3	43	6	AR111858	AR111858 Sequence	737	12.2	43.6	20	6	AR038252	AR03825
44.3	43	6	AR338255	AR338255 Sequence	738	12.2	43.6	20	6	AR165127	AR16512
44.3	43	6	BD132485	BD132485 Binding m	739	12.2	43.6	20	6	AR177577	AR17757
44.3	43	6	BD242809	BD242809 Method an	740	12.2	43.6	20	6	BD244938	BD24493
44.3	44	6	AX580284	AX580284 Sequence	C 741	12.2	43.6	20	6	AR314563	AR31456
44.3	44	6	AX786449	AX786449 Sequence	742	12.2	43.6	20	6	AX546321	AX54632
44.3	44	6	BD188253	BD188253 bHLH-PAS	743	12.2	43.6	20	6	AX546411	AX54641
44.3	45	6	I24864	I24864 Sequence 35	744	12.2	43.6	21	6	AR135573	AR13557
44.3	46	6	I72685	I72685 Sequence 47	C 745	12.2	43.6	21	6	AX096165	AX09616
44.3	46	6	AX496415	AX496415 Sequence	746	12.2	43.6	21	6	AX664942	AX66494
44.3	46	6	AX769580	AX769580 Sequence	C 747	12.2	43.6	22	6	A32631	A32631
44.3	47	6	AR289651	AR289651 Sequence	C 748	12.2	43.6	22	6	AR097776	AR09777
44.3	47	6	AR290206	AR290206 Sequence	749	12.2	43.6	22	6	AR264253	AR26425
44.3	49	6	BD142681	BD142681 Polypepti	C 750	12.2	43.6	22	6	AX743852	AX74385
44.3	50	6	AR079798	AR079798 Sequence	751	12.2	43.6	23	6	AR134781	AR13478
44.3	50	6	AR081328	AR081328 Sequence	C 752	12.2	43.6	23	6	AR134782	AR13478
44.3	50	6	AR146488	AR146488 Sequence	C 753	12.2	43.6	23	6	AX078386	AX07838
44.3	50	6	AR170688	AR170688 Sequence	754	12.2	43.6	23	6	AX078387	AX07838
44.3	50	6	AR218542	AR218542 Sequence	C 755	12.2	43.6	23	6	AX429382	AX42938
44.3	50	6	AX235222	AX235222 Sequence	C 756	12.2	43.6	24	6	A20717	A20717
44.3	50	6	AX657048	AX657048 Sequence	757	12.2	43.6	25	6	BD233809	BD23380
44.3	51	6	AR182334	AR182334 Sequence	C 758	12.2	43.6	25	6	AR281763	AR28176
44.3	51	6	AR350399	AR350399 Sequence	C 759	12.2	43.6	25	6	AX532766	AX53276
44.3	51	6	AR409163	AR409163 Sequence	C 760	12.2	43.6	25	6	AX532767	AX53276
44.3	51	6	AX116045	AX116045 Sequence	C 761	12.2	43.6	25	6	AX611015	AX61101
44.3	51	6	AX157463	AX157463 Sequence	C 762	12.2	43.6	25	6	AX615694	AX61569
44.3	51	6	AX157465	AX157465 Sequence	763	12.2	43.6	25	6	AX650266	AX65026
44.3	51	6	AX157466	AX157466 Sequence	764	12.2	43.6	25	6	AX650267	AX65026
44.3	51	6	AX159444	AX159444 Sequence	765	12.2	43.6	25	6	AX650268	AX65026
44.3	51	6	AX163192	AX163192 Sequence	766	12.2	43.6	25	6	AX650269	AX65026
44.3	51	6	AX163332	AX163332 Sequence	C 767	12.2	43.6	25	6	AX650270	AX65027
44.3	52	6	AR077800	AR077800 Sequence	768	12.2	43.6	25	6	AX650271	AX65027
44.3	52	6	BD227169	BD227169 Protease	C 769	12.2	43.6	25	6	AX650272	AX65027
44.3	52	6	AR368745	AR368745 Sequence	770	12.2	43.6	25	6	AX650273	AX65027
44.3	52	6	AR392700	AR392700 Sequence	C 771	12.2	43.6	25	6	AX650274	AX65027
44.3	52	6	AX074060	AX074060 Sequence	C 772	12.2	43.6	27	6	AR030841	AR03084
44.3	52	6	AX657918	AX657918 Sequence	C 773	12.2	43.6	27	6	BD233807	BD23380
44.3	53	11	BX322447	BX322447 Arabidops	C 774	12.2	43.6	27	6	I82800	I82800
44.3	54	6	AR051072	AR051072 Sequence	C 775	12.2	43.6	27	6	AR187689	AR18768
44.3	54	6	AR430286	AR430286 Sequence	C 776	12.2	43.6	27	6	AR187968	AR18796
44.3	54	6	AX008517	AX008517 Sequence	C 777	12.2	43.6	27	6	AR189139	AR18913
44.3	54	6	BD218399	BD218399 Newcastle	C 778	12.2	43.6	27	6	AR189237	AR18923
44.3	56	6	AR146487	AR146487 Sequence	C 779	12.2	43.6	27	6	AR281761	AR28176
44.3	57	6	AX286674	AX286674 Sequence	C 780	12.2	43.6	27	6	AR402829	AR40282
44.3	57	6	AX899395	AX899395 Sequence	C 781	12.2	43.6	27	6	BD068329	BD06832
44.3	57	6	BD034928	BD034928 Sequence	C 782	12.2	43.6	28	6	AR257259	AR25725
44.3	58	6	AR169957	AR169957 Sequence	C 783	12.2	43.6	28	6	AX351792	AX35179
44.3	58	6	AR411922	AR411922 Sequence	C 784	12.2	43.6	28	6	AX643651	AX64365
44.3	58	6	AR428092	AR428092 Sequence	785	12.2	43.6	28	6	AX643916	AX64391
44.3	58	6	AX711190	AX711190 Sequence	C 786	12.2	43.6	29	6	AR027755	AR02775
44.3	60	6	AR022509	AR022509 Sequence	787	12.2	43.6	29	6	AR029159	AR02915
44.3	60	6	AR068987	AR068987 Sequence	C 788	12.2	43.6	29	6	AR036543	AR03654
44.3	60	6	AR135014	AR135014 Sequence	789	12.2	43.6	29	6	AR096076	AR09607
44.3	60	6	AR141843	AR141843 Sequence	C 790	12.2	43.6	29	6	AR111943	AR11194
44.3	60	6	AR143360	AR143360 Sequence	791	12.2	43.6	29	6	AR124840	AR12484
44.3	60	6	AR151969	AR151969 Sequence	C 792	12.2	43.6	29	6	AR135288	AR13528
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44.3	60	6	I36449	I36449 Sequence 16	C 794	12.2	43.6	29	6	AR179520	AR17952
44.3	60	6	I88149	I88149 Sequence 16	C 795	12.2	43.6	29	6	BD252540	BD25254

43.6	29	6	I31657	I31657 Sequence 8	869	12.2	43.6	45	6	AX306498	AX306498
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43.6	29	6	AR231424	AR231424 Sequence	872	12.2	43.6	46	6	AR134780	AR134780
43.6	29	6	AR412360	AR412360 Sequence	C 873	12.2	43.6	46	6	I71488	I71488
43.6	29	6	AX306927	AX306927 Sequence	874	12.2	43.6	46	6	AX078384	AX078384
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43.6	29	6	BD222593	BD222593 Aminoxy-	C 876	12.2	43.6	47	6	AR289156	AR289156
43.6	30	6	AX128327	AX128327 Sequence	C 877	12.2	43.6	47	6	AR290134	AR290134
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43.6	30	6	AX793675	AX793675 Sequence	C 884	12.2	43.6	48	6	AX426589	AX426589
43.6	30	6	AX793938	AX793938 Sequence	C 885	12.2	43.6	49	6	AR372730	AR372730
43.6	32	6	BD261370	BD261370 Plants, s	C 886	12.2	43.6	49	6	AX167839	AX167839
43.6	32	6	AR184306	AR184306 Sequence	C 887	12.2	43.6	49	6	BD095963	BD095963
43.6	32	6	AR431248	AR431248 Sequence	C 888	12.2	43.6	49	8	AJ592187	AJ592187
43.6	32	6	BD132771	BD132771 Fatty aci	C 889	12.2	43.6	49	8	AJ599619	AJ599619
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43.6	34	6	AR309976	AR309976 Sequence	C 895	12.2	43.6	51	6	AX156775	AX156775
43.6	35	6	AR171495	AR171495 Sequence	C 896	12.2	43.6	51	6	AX190092	AX190092
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43.6	35	6	AX280684	AX280684 Sequence	C 901	12.2	43.6	54	6	AR076456	AR076456
43.6	35	6	BD005515	BD005515 Compositi	C 902	12.2	43.6	54	6	AR124693	AR124693
43.6	35	6	BD102805	BD102805 Process f	C 903	12.2	43.6	54	6	BD247210	BD247210
43.6	35	6	BD128318	BD128318 Endostati	C 904	12.2	43.6	54	6	I62702	I62702
43.6	36	6	AR106488	AR106488 Sequence	C 905	12.2	43.6	54	6	AR208219	AR208219
43.6	36	6	AX280683	AX280683 Sequence	C 906	12.2	43.6	54	6	AR217573	AR217573
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43.6	39	6	AR011588	AR011588 Sequence	C 909	12.2	43.6	56	6	AX184290	AX184290
43.6	39	6	AR028002	AR028002 Sequence	910	12.2	43.6	57	6	AX17360	AX17360
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43.6	40	6	BD266519	BD266519 Universal	C 916	12.2	43.6	59	6	AR013892	AR013892
43.6	40	6	AR409827	AR409827 Sequence	C 917	12.2	43.6	59	6	AR015952	AR015952
43.6	40	6	AX460353	AX460353 Sequence	C 918	12.2	43.6	59	6	AR033846	AR033846
43.6	40	6	AX460354	AX460354 Sequence	C 919	12.2	43.6	59	6	AR042506	AR042506
43.6	40	6	AX525973	AX525973 Sequence	C 920	12.2	43.6	59	6	AR052894	AR052894
43.6	41	6	A61793	A61793 Sequence 16	921	12.2	43.6	59	6	AR054257	AR054257
43.6	41	6	AR109155	AR109155 Sequence	C 922	12.2	43.6	59	6	AR054459	AR054459
43.6	41	6	E14310	E14310 PCR primer	C 923	12.2	43.6	59	6	AR058386	AR058386
43.6	41	6	AR200810	AR200810 Sequence	C 924	12.2	43.6	59	6	AR088212	AR088212
43.6	41	6	AX059985	AX059985 Sequence	C 925	12.2	43.6	60	6	AR118272	AR118272
43.6	41	6	AX518563	AX518563 Sequence	926	12.2	43.6	60	6	E22144	E22144
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43.6	42	6	BD266457	BD266457 Universal	C 928	12.2	43.6	60	6	AR363025	AR363025
43.6	42	6	AX611705	AX611705 Sequence	C 929	12.2	43.6	60	6	AR372280	AR372280
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43.6	44	6	AX683012	AX683012 Sequence	C 931	12.2	43.6	60	6	BD130792	BD130792
43.6	45	6	AR012681	AR012681 Sequence	932	12	42.9	20	6	AR118941	AR118941
43.6	45	6	AR013852	AR013852 Sequence	933	12	42.9	20	6	E14236	E14236
43.6	45	6	AR033806	AR033806 Sequence	C 934	12	42.9	20	6	AR307957	AR307957
43.6	45	6	AR042466	AR042466 Sequence	C 935	12	42.9	20	6	AR336975	AR336975
43.6	45	6	AR058346	AR058346 Sequence	C 936	12	42.9	20	6	AX462563	AX462563
43.6	45	6	AR088172	AR088172 Sequence	937	12	42.9	21	6	AR067054	AR067054
43.6	45	6	I25047	I25047 Sequence 21	C 938	12	42.9	21	6	AR084556	AR084556
43.6	45	6	I30509	I30509 Sequence 21	939	12	42.9	21	6	AR084560	AR084560
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43.6	45	6			C 941	12	42.9	21	6	AR084597	AR084597

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 42.9 23 6 AX147042 Sequence
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 42.9 24 6 AX446405 Sequence
 42.9 25 6 AX015836 Sequence
 42.9 25 6 AX203144 Sequence
 42.9 25 6 AX609742 Sequence
 42.9 25 6 BD205326 Materials
 42.9 26 6 BD016922 Novel pol
 42.9 27 6 A75720 Sequence 10
 42.9 27 6 E06840 Oligonucleo
 42.9 27 6 AR187969 Sequence
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 42.9 28 8 ATH527112 Arabidops
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 42.9 30 6 AR079764 Sequence
 42.9 30 6 AR081294 Sequence
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 42.9 30 6 AX793041 Sequence
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 42.9 31 6 AR338155 Sequence
 42.9 31 6 BD062098 Alternati
 42.9 32 6 A44208 Sequence 13
 42.9 32 6 A65630 Sequence 15
 42.9 32 6 AR020956 Sequence

ALIGNMENTS

1634 6 from Patent WO9856936. linear PAT 10-MAR-2000
 1634 20 bp DNA
 1634.1 GI:7241763

Identified
 identified

unclassified.
 1 (bases 1 to 20)
 Damert, A. and Plate, K.
 REGULATORY SEQUENCES INVOLVED IN HYPOXIA REGULATED GENE
 AND USE THEREOF
 Patent: WO 9856936-A 6-19-DEC-1998;
 MAX PLANCK GESELLSCHAFT (DE); DAMERT ANNETTE (DE)
 Location/Qualifiers
 1..20
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN
 Query Match 71.4%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0;

QY 7 ATCCTCTGCATGTCAGGTC 26
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 Db 1 ATCCTCTGCATGTCAGGTC 20

RESULT 2
 LOCUS AX002137 20 bp DNA linear PAT
 DEFINITION Sequence 14 from Patent WO9855638.
 ACCESSION AX002137
 VERSION AX002137.1 GI:7241852
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 1 (bases 1 to 20)
 Breier, G. and Risaau, W.
 REGULATORY SEQUENCES CAPABLE OF CONFERRING EXPRESSION O
 HETEROLOGOUS DNA SEQUENCE IN ENDOTHELIAL CELLS IN VIVO
 THEREOF
 Patent: WO 9855638-A 14 10-DEC-1998;
 MAX PLANCK GESELLSCHAFT (DE); BREIER GEORG (DE)
 Location/Qualifiers
 1..20
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN
 Query Match 71.4%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0;

QY 7 ATCCTCTGCATGTCAGGTC 26
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 Db 1 ATCCTCTGCATGTCAGGTC 20

RESULT 3
 LOCUS AX816396 20 bp DNA linear PAT
 DEFINITION Sequence 25 from Patent WO03066867.
 ACCESSION AX816396
 VERSION AX816396.1 GI:39646871
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 1
 Andreas, S. and Faust, N.
 Genetically engineered phic31minus; integrase genes
 Patent: WO 03066867-A 25 14-AUG-2003;
 ARTEMIS Pharmaceuticals GmbH (DE)
 Location/Qualifiers
 1..20

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence:
oligonucleotide"

71.4%; Score 20; DB 6; Length 20;
Similarity 100.0%; Pred. No. 2.6e+02;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TCTCTGCATGGTCAGGTC 26
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TCTCTGCATGGTCAGGTC 20

95919 20 bp DNA linear PAT 17-JUL-2003
Library sequences capable of conferring expression of a
prologous DNA sequence in endothelial cells in vivo and uses
reof.

35919
35913.1 GI:33005689
2002511750-A/14.

Identified
classified.

(bases 1 to 20)

er.G., Rissau, W. and Ronicke, V.

Library sequences capable of conferring expression of a
prologous DNA sequence in endothelial cells in vivo and uses
int: JP 2002511750-A 14 16-APR-2002;

PLANCK GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN EV

Unidentified

JP 2002511750-A/14

16-APR-2002

03-JUN-1998 JP 1999501504

03-JUN-1997 EP 97108959.4

GEORG BREIER, WERNER RISSAU, VOLKER RONICKE

C12N15/85, C12N15/12, C12N15/19, C07K14/47, C07K14/52, C12N15/58,

C12N9/72,

C12N15/53, C12N9/02, C12N15/23, C07K14/57, C12N15/16, C07K14/58, PC

2N5/10,

A61K48/00

Strandedness: Single;

Topology: linear;

/desc = 'oligonucleotide'

Key Location/Qualifiers

source 1..20

Location/Qualifiers

1..20

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71.4%; Score 20; DB 6; Length 20;
Similarity 100.0%; Pred. No. 2.6e+02;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TCTCTGCATGGTCAGGTC 26

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TCTCTGCATGGTCAGGTC 20

33 30 bp DNA linear PAT 26-JAN-2000

ance 9 from Patent WO9910500.

33.1 GI:6781697

KEYWORDS
SOURCE
ORGANISM

unidentified
unidentified
unclassified.

REFERENCE
1 (bases 1 to 30)

Schlichter, U. and Steinbiss, H.

NUCLEIC ACID MOLECULES CODING FOR A CYSTEINE PROTEINASE

AUTHORS
ORIGIN AND THEIR REGULATING REGIONS

JOURNAL
Patent: WO 9910500-A 9 04-MAR-1999;

FEATURES
MAX PLANCK GESELLSCHAFT (DE); SCHLICHTER URSULA (DE)

source
1..30

Location/Qualifiers

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

ORIGIN

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QY 3 CATCATCTCTCGATGGTCAGGTCAT 28

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Db 3 CATCTCATCTCGAGGTCAGGTCCT 28

RESULT 6

AX538397/c

LOCUS

AX538397 Sequence 177 from Patent WO02072846.

ACCESSION

AX538397

VERSION

AX538397.1 GI:25270733

KEYWORDS

synthetic construct

synthetic construct

artificial sequences.

ORGANISM

REFERENCE

1

AUTHORS

Dr. D. J. P. and Tiraby, G.

TITLE

Synthetic genes and bacterial plasmids devoid of cpg

JOURNAL

Patent: WO 02072846-A 177 19-SEP-2002;

KEYWORDS

CAYLA (FR)

FEATURES

Location/Qualifiers

1..40

/organism="synthetic construct"

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/note="assembling oligo for CpG-free LacZ"

ORIGIN

Query Match 61.4%; Score 17.2; DB 6; Length 40;

Best Local Similarity 86.4%; Pred. No. 5.5e+03;

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QY 1 AGCATCATCTCTCGATGGTCAT 22

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Db 23 AGCACCACCTCTCGATGGACA 2

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RESULT 7

AX538396

LOCUS

AX538396 Sequence 176 from Patent WO02072846.

ACCESSION

AX538396

VERSION

AX538396.1 GI:25270732

KEYWORDS

synthetic construct

synthetic construct

artificial sequences.

ORGANISM

REFERENCE

1

AUTHORS

Dr. D. J. P. and Tiraby, G.

TITLE

Synthetic genes and bacterial plasmids devoid of cpg

JOURNAL

Patent: WO 02072846-A 176 19-SEP-2002;

CAYLA (FR)

Location/Qualifiers

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 /mol_type="unassigned DNA"
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ACCACTCTCTGCATGTCAGGTCA 25

717 29 bp DNA linear PAT 15-OCT-1999
 nence 7 from Patent WO9322440.
 717 GI:6065688

identified
 identified
 lassified.
 (bases 1 to 29)

..B. and Yap,E.

IA SEQUENCE OF DENGUE VIRUS SEROTYPE 1 (SINGAPORE STRAIN)

ent: WO 9322440-A 7 11-NOV-1993;

BOON HUAN (SG); YAP EU HIAN (SG)

Location/Qualifiers

1..29

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

Similarity 57.1%; Score 16; DB 6; Length 29;
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;

GCATCATCCTCTGCATGTCAGG 24

TCAGAAATTCCTGCAGGGTCAGG 25

337 29 bp DNA linear PAT 29-SEP-1997
 onucleotide for PCR.
 337

337.1 GI:2175019

1994070760-A/6.

thetic construct

thetic construct

ificial sequences.

(bases 1 to 29)

irin,F., Buunnfuan,T., Iuuhian,Y., Youuchiyan,C. and Innuii,T.

SUE VIRUS

ent: JP 1994070760-A 6 15-MAR-1994;

VRIN FUU, BUUNNFUAN TAN, IUUHIAN YAFU, YOUUCHIYON CHIVAN, IN UII

Artificial gene

Artificial sequence; Genes.

JP 1994070760-A/6

15-MAR-1994

30-APR-1993 JP 1993127968

30-APR-1992 JP 92P 137717

JIARIN FUU, BUUNNFUAN TAN, IUUHIAN YAFU, YOUUCHIYON CHIVAN,

INNUII TAN

C12N7/00,A61K39/12,C07K7/10,C07K13/00,C12N1/21,C12N5/10, PC

C12N7/04,C12N15/40,
 PC C12N15/62,C12P21/02,G01N33/53,G01N33/569,(C12N1/2

PC (C12P21/02,

PC C12R1:19),C07K99:00;

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FEATURES

source

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/db_xref="taxon:32630"

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Best Local Similarity 79.2%; Pred.No. 1.9e+04;

Matches 19; Conservative 0; Mismatches 5; Indels 0;

Qy 1 AGCATCATCCTCTGCATGTCAGG 24

2 ATCAGAATTCCTGCAGGGTCAGG 25

RESULT 10

AX328821

LOCUS

AX328821

DEFINITION

Sequence 318 from Patent EP1164203.

AX328821

ACCESSION

AX328821

VERSION

AX328821.1

GI:18102020

KEYWORDS

unidentified

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1

AUTHORS

Koester,H., Little,D.P., Braun,A., Jurinke,C., van den

Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,F.

Dna diagnostics based on mass spectrometry

Patent: EP 1164203-A 318 19-DEC-2001;

SEQUENOM, INC. (US)

FEATURES

source

1..42

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/db_xref="taxon:32644"

Query Match 57.1%; Score 16; DB 6; Length 42;

Best Local Similarity 79.2%; Pred.No. 2e+04;

Matches 19; Conservative 0; Mismatches 5; Indels 0;

Qy 4 ATCATCCTCTGCATGTCAGGTCA 27

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RESULT 11

BD132386

LOCUS

BD132386

DEFINITION

DNA diagnosis method based on mass spectrometry.

BD132386

ACCESSION

BD132386.1

GI:23227331

VERSION

JP 2002507883-A/318.

KEYWORDS

synthetic construct

SOURCE

synthetic construct

artificial sequences.

ORGANISM

1 (bases 1 to 42)

REFERENCE

1

AUTHORS

Koester,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,

Boom,D.V.D., Jurinke,C. and Rupert,A.

DNA diagnosis method based on mass spectrometry

Patent: JP 2002507883-A 318 12-MAR-2002;

SEQUENOM INC

TITLE

JP 2002507883-A/318

JOURNAL

PN JP 2002507883-A/318

COMMENT

PD 12-MAR-2002

PF 06-NOV-1997 JP 1998521832

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06-NOV-1996 US 08/744481.06-NOV-1996 US 08/746036 PR
NOV-1996 US 08/746055.06-NOV-1996 US 08/744590 PR
JAN-1997 US 08/786988.23-JAN-1997 US 08/787639 PR
SEP-1997 US 08/933752.08-OCT-1997 US 08/947801 PI HUBERT
PER, DANIEL P LITTLE, ANDREAS BRAUN, DAVID M LOUGH, PI GUOBING
NG,
DIRK VAN DEN BOOM, CHRISTIAN JURINKE, ANDREAS RUPERT PC
21/68, C07H21/00, C07F9/24
Strandedness: Single;
Topology: Unknown;
Key Location/Qualifiers.
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  /mol_type="genomic DNA"
  /db_xref="taxon:32630"
  57.1%; Score 16; DB 6; Length 42;
  ilarity 79.2%; Pred. No. 2e+04;
  Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  CATCCTCTGCATGTCAGGTCA 27
  CATCACTGGAGATCAGGTCA 24

9517
ence 14 from patent US 5891669.
9517
9517.1 GI:7220405
OWN.
OWN.
assified.
ases 1 to 30)
en,E.Bech., Cherry,J.R. and Elrod,S.L.
ods for producing polypeptides in respiratory-deficient cells
nt: US 5891669-A 14 06-APR-1999;
Location/Qualifiers
  1..30
  /organism="unknown"
  /mol_type="unassigned DNA"
  55.7%; Score 15.6; DB 6; Length 30;
  ilarity 81.8%; Pred. No. 3e+04;
  Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  CATCATCCTCTGCATGTCATCA 22
  CGTCATCCTCTGCTTCGTCA 5

5684
ods for producing polypeptides in respiratory-deficient cells.
5684
5684.1 GI:33005454
002510965-A/12.
hetic construct
hetic construct
ficial sequences.
ases 1 to 30)
en,E.B., Cherry,J.R. and Elrod,S.L.
ods for producing polypeptides in respiratory-deficient cells
nt: JP 2002510965-A 13 09-APR-2002;
NORDISK AS,NOVO NORDISK BIOTECH INC
Artificial Sequence
JP 2002510965-A/12

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PD 09-APR-2002
PF 17-MAR-1998 JP 1998540692
PR 17-MAR-1997 US 08/819458
PI EUNER BECH JENSEN,JOEL R CHERRY,SUSAN L ELROD PC
CL2N15/64,CL2P21/02,CL2N1/14//CL2R1/69
CC Aspergillus oryzae
FH Key Location/Qualifiers
FT source 1..30
  /organism="Artificial Sequence".
  Location/Qualifiers
  1..30
  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"
  55.7%; Score 15.6; DB 6; Length 30;
  Best Local Similarity 81.8%; Pred. No. 3e+04;
  Matches 18; Conservative 0; Mismatches 4; Indels 0;
  QY 1 AGCATCATCCTCTGCATGTCATCA 22
  Db 26 ATCGTCATCCTCTGCTTCGTCA 5

RESULT 14
BD266770
LOCUS
DEFINITION
  Proteins that bind angiogenesis-inhibiting proteins, con
  and methods of use thereof.
ACCESSION
  BD266770
VERSION
  BD266770.1 GI:33076538
KEYWORDS
  JP 2002532068-A/31.
SOURCE
  synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
REFERENCE
  1 (bases 1 to 33)
  Macdonald,N.J. and Sim,K.L.
  Proteins that bind angiogenesis-inhibiting proteins, con
  and methods of use thereof
  Patent: JP 2002532068-A 31 02-OCT-2002;
  ENTREMED INC
COMMENT
  OS Artificial Sequence
  PN JP 2002532068-A/31
  PD 02-OCT-2002
  PF 06-DEC-1999 JP 2000585271
  PR 04-DEC-1998 US 09/206059
  PI NICHOLAS J MACDONALD,KIM LEE SIM
  PC CL2N15/09,A61K38/00,A61P9/00,A61P27/02,A61P29/00,A6
  A61P43/00,
  PC C07K14/705,G01N33/15,G01N33/50,G01N33/53,G01N33/566//A61
  A61K45/00,
  PC A61K48/00,CL2N15/00,A61K37/02
  CC Synthetic binding peptide
  FH Key Location/Qualifiers
  FT source 1..33
  /organism="Artificial Sequence".
  Location/Qualifiers
  1..33
  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"
  54.3%; Score 15.2; DB 6; Length 33;
  Best Local Similarity 85.0%; Pred. No. 4.6e+04;
  Matches 17; Conservative 0; Mismatches 3; Indels 0;
  QY 1 AGCATCATCCTCTGCATGTT 20
  Db 5 AGCTCTCATCTGCATGTT 24

```

195703 33 bp DNA linear PAT 18-MAY-2002
 195703 71 from Patent WO0193897.
 195703 1 GI:21066500

thetic construct
 thetic construct
 icial sequences.

a,K.L. and Macdonald,N.J.
 iostatatin and endostatin binding proteins and methods of use
 :remed, inc. (US)
 :WO 0193897-A 71 13-DEC-2001;

Location/Qualifiers
 1. 33
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="binding molecule"

54.3%; Score 15.2; DB 6; Length 33;
 milarity 85.0%; Pred. No. 4.6e+04;
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

GCATCATCTCTGTCAGTGGT 20
 |||||
 GCCTCTCTGTCAGTGGT 24

296 35 bp DNA linear PAT 12-NOV-1993
 296 leotide sequence 21 from patent number EP0274560.

296.1 GI:492922

identified
 identified
 lassified.

(bases 1 to 35)
 iguchi,T., Yamada,G., Hamuro,J., Taki,S., Matsui,H. and
 hima,N.
 an hematopoietic cell growth potentiating factor
 ent: EP 0274560-A 21 20-JUL-1988;
 NOMOTO CO., INC.; Taniguchi, Tadatsugu
 Location/Qualifiers

1. 35
 /organism="unidentified"
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 /db_xref="taxon:32644"

54.3%; Score 15.2; DB 6; Length 35;
 milarity 71.4%; Pred. No. 4.6e+04;
 Conservative 0; Mismatches 8; Indels 0; Gaps 0;

GCATCATCTCTGTCAGTGGT 28
 |||||
 GCAGCTCTCTGTCAGGTCATGGCTT 33

037 38 bp DNA linear PAT 12-NOV-1993
 leotide sequence 2 from patent number EP0274560.

037.1 GI:492397

identified

ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 38)
 AUTHORS Taniguchi,T., Yamada,G., Hamuro,J., Taki,S., Matsui,H.
 Kashima,N.
 TITLE Human hematopoietic cell growth potentiating factor
 JOURNAL Patent: EP 0274560-A 2 20-JUL-1988;
 AJINOMOTO CO., INC.; Taniguchi, Tadatsugu
 FEATURES Location/Qualifiers
 source 1. 38
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

Query Match 54.3%; Score 15.2; DB 6; Length 38;
 Best Local Similarity 71.4%; Pred. No. 4.6e+04;
 Matches 20; Conservative 0; Mismatches 8; Indels 0;

Qy 1 AGCATCATCTCTGTCAGTGGTCAAT 28
 |||||
 Db 6 AGCAGCTCTCTGTCAGGTCATGGCTT 33

RESULT 18
 A11036/c
 LOCUS A11036 41 bp DNA linear PAT
 DEFINITION Nucleotide sequence 1 from patent number EP0274560.
 ACCESSION A11036
 VERSION A11036.1 GI:492396
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 41)
 AUTHORS Taniguchi,T., Yamada,G., Hamuro,J., Taki,S., Matsui,H.
 Kashima,N.
 TITLE Human hematopoietic cell growth potentiating factor
 JOURNAL Patent: EP 0274560-A 1 20-JUL-1988;
 AJINOMOTO CO., INC.; Taniguchi, Tadatsugu
 FEATURES Location/Qualifiers

source 1. 41
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 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORGANISM
 Query Match 54.3%; Score 15.2; DB 6; Length 41;
 Best Local Similarity 71.4%; Pred. No. 4.7e+04;
 Matches 20; Conservative 0; Mismatches 8; Indels 0;

Qy 1 AGCATCATCTCTGTCAGTGGTCAAT 28
 |||||
 Db 32 AGCAGCTCTCTGTCAGGTCATGGCTT 5

RESULT 19
 A11295/c
 LOCUS A11295 41 bp DNA linear PAT
 DEFINITION Nucleotide sequence 20 from patent number EP0274560.
 ACCESSION A11295
 VERSION A11295.1 GI:492403
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 41)
 AUTHORS Taniguchi,T., Yamada,G., Hamuro,J., Taki,S., Matsui,H. &
 Kashima,N.
 TITLE Human hematopoietic cell growth potentiating factor
 JOURNAL Patent: EP 0274560-A 20-JUL-1988;
 AJINOMOTO CO., INC.; Taniguchi, Tadatsugu
 FEATURES Location/Qualifiers

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1. .41
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

milarity 54.3%; Score 15.2; DB 6; Length 41;
Conservative 0; Mismatches 8; Indels 0; Gaps 0;

GCATCATCTCTGCATGGTCAGGTCAT 28
|||||
GAGCCTCTTCAGCAGGTCATGGCTT 5

475
mer.
475
475.1 GI:5710158
1998072495-A/6.
identified
identified
classified.
(bases 1 to 56)
abayashi,T. and Sakano,S.
UNITY-RELATED FACTOR
nt: JP 1998072495-A 6 17-MAR-1998;
H CHEM IND CO LTD
None
Artificial sequences.
JP 1998072495-A/6
17-MAR-1998
11-JUN-1997 JP 1997153218
13-JUN-1996 JP 96P 152362
MIYABAYASHI TOMOYUKI, SAKANO SEIJI
C07K14/47,C07H21/04,C07K16/18,C12N5/10,C12N15/09, PC
21/02//A61K38/00,
C12P21/08, (C12N5/10, C12R1/91), (C12P21/02, C12R1/91), (C12P21/08,
C12R1/91);
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topology: Linear;
hypotheical: No;
Key Location/Qualifiers
source 1. .56
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Location/Qualifiers
1. .56
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/db_xref="taxon:32644"

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Conservative 0; Mismatches 8; Indels 0; Gaps 0;

CATCATCTCTGCATGGTCAGGTCAT 28
|||||
CATCATCATCTTTATTAATCGGTCCT 42

7977
nce 34 from Patent WO0190747.
7977
7977.1 GI:18098132
etic construct
etic construct

```

artificial sequences.

REFERENCE 1
AUTHORS Rhode, P., Wittman, V., Weidanz, J. A., Burkhardt, M., Card, Tal, R., Acevedo, J. and Wong, H. C.
TITLE Modulation of t-cell receptor interactions
JOURNAL Patent: WO 0190747-A 34 29-NOV-2001;
Sunol Molecular Corporation (US)
FEATURES
source 1. .58
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN

Query Match 54.3%; Score 15.2; DB 6; Length 58;
Best Local Similarity 85.0%; Pred. No. 4.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0;

QY 6 CATCTCTCTGCATGGTCAGGT 25
|||||
DB 53 CATCTCTCTGTGTGTCAGGT 34
|||||

RESULT 22
AX254656
LOCUS AX254656 44 bp DNA linear PAT
DEFINITION Sequence 12 from Patent WO0168818.
ACCESSION AX254656
VERSION AX254656.1 GI:16074328
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Steinkuhler, C. I., Pallaro, M. I. and Lahm, A. I.
TITLE Hcv ns2/3 fragments and uses thereof
JOURNAL Patent: WO 0168818-A 12 20-SEP-2001;
Istituto di Ricerche di Biologia Molecolare P. Angelelli
FEATURES
source 1. .44
Location/Qualifiers
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Primer"

ORIGIN

Query Match 53.6%; Score 15; DB 6; Length 44;
Best Local Similarity 78.3%; Pred. No. 5.8e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0;

QY 2 GCATCATCTCTGCATGGTCAGG 24
|||||
DB 2 GCATCATCATCATCATCATCAGG 24
|||||

RESULT 23
BD002886/c
LOCUS BD002886 31 bp DNA linear PAT
DEFINITION Gene composition and method.
ACCESSION BD002886
VERSION BD002886.1 GI:18630847
KEYWORDS JP 2000245487-A/552.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 31)
AUTHORS Sha, N., Walinton, J. and Patel, N.
TITLE Gene composition and method
JOURNAL Patent: JP 2000245487-A 552 12-SEP-2000;
AFIMETRICS INC
COMMENT OS Unknown
EN JP 2000245487-A/552

12-SEP-2000
 27-JAN-2000 JP 2000019392
 27-JAN-1999 US 09/238,402
 NIRA SHA, JANET WALINTON, NIRA PATEL
 C12N15/09, C12Q1/68, C12N15/00

Key Location/Qualifiers
 source 1..31
 /organism="Unknown"

Location/Qualifiers
 1..31
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

52.9%; Score 14.8; DB 6; Length 31;
 milarity 80.0%; Pred. No. 7e+04;

Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GCATCATCTCTGCATGGT 20
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 GCCTCTGCTCTGCATTGT 3

618 40 bp DNA linear PAT 21-JAN-2000
 uence 47 from Patent WO9849324.

618.1 GI:6732870

Identified
 Identified
 Identified
 (bases 1 to 40)
 his, G.

BOHYDRATE-DEFICIENT GLYCOPROTEIN SYNDROME TYPE I

art: WO 9849324-A 47 05-NOV-1998;

THIS GERT (BE); GENZYME LTD (GB)

Location/Qualifiers

1..40
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

52.9%; Score 14.8; DB 6; Length 40;
 milarity 73.1%; Pred. No. 7.1e+04;

Conservative 0; Mismatches 7; Indels 0; Gaps 0;

TATCATCTCTGCATGGTCAGTCA 27
 |||:|||||
 TTCTTGCTGAGATGGTGGCCA 4

38134 46 bp DNA linear PAT 14-FEB-2003
 ence 408 from Patent WO0244994.

38134
 38134.1 GI:28398308

thetic construct
 thetic construct
 ificial sequences.

ver A., Brow, M.A., Cracauer, R.F., Fors, L., Granske, R., de arruda
 ig, M., Kurensky, D., Luedtke, C., Lukowiak, A.A., Lyamichev, V.,
 B.P., Reimer, N.B., Roeven, R.T., Skrzypczynski, Z., Ziarno, W.A.,
 rford, S., Stump, S. and Viegut, D.D.
 ems and method for detection assay production and sale
 nt: WO 0244994-A 408 06-JUN-2002;

THIRD WAVE TECHNOLOGIES, INC. (US)
 Location/Qualifiers
 1..46
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 52.9%; Score 14.8; DB 6; Length 46;
 Best Local Similarity 73.1%; Pred. No. 7.2e+04;
 Matches 19; Conservative 0; Mismatches 7; Indels 0;

QY 1 AGCATCATCTCTGCATGGTCAGGTC 26
 |||:|||||
 Db 26 AGCATCATTTATTTGCAGACAGGAC 1

RESULT 26
 AR148167

LOCUS 50 bp DNA linear PAT
 DEFINITION Sequence 13 from patent US 6225063.

ACCESSION AR148167

VERSION AR148167.1 GI:15112257

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 50)

AUTHORS Khvorova, A. and Varus, M.

TITLE RNA channels in biological membranes

JOURNAL Patent: US 6225063-A 13 01-MAY-2001;

FEATURES Location/Qualifiers

source 1..50

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 52.9%; Score 14.8; DB 6; Length 50;
 Best Local Similarity 73.1%; Pred. No. 7.2e+04;
 Matches 19; Conservative 0; Mismatches 7; Indels 0;

QY 1 AGCATCATCTCTGCATGGTCAGGTC 26
 |||:|||||
 Db 7 ATCTTAATCTCTGCGTGGTCAGGTC 32

RESULT 27
 AX157925

LOCUS 51 bp DNA linear PAT
 DEFINITION Sequence 1253 from Patent WO0140521.

ACCESSION AX157925

VERSION AX157925.1 GI:14539256

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Hos

1 Shimkets, R.A. and Leach, M.

Nucleic acids containing single nucleotide polymorphisms

Methods of use thereof

Patent: WO 0140521-A 1253 07-JUN-2001;

Curagen Corporation (US)

FEATURES Location/Qualifiers

source 1..51

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

26

misc_feature /note="1 of 2 allelic variants (1254 is other e

Accession number cg28473092"

ORIGIN

52.1%; Score 14.6; DB 6; Length 40;
 milarity 81.0%; Pred. No. 8.9e+04;
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCATCTCTGTCATGGTCA 22
 ||| ||||| ||||| |||||
 ACCTGCTCTACATGGTCA 13

34368 45 bp DNA linear PAT 11-SEP-2001
 uence 18 from Patent WO0162942.

34368
 34368.1 GI:15593369

thetic construct
 thetic construct
 ificial sequences.

talo, K.M. and Jeltsch, M.M.
 erials and methods involving hybrid vascular endothelial growth
 tor dnas and proteins and screening methods for modulators
 ent: WO 0162942-A 18 30-AUG-2001;
 NIG INSTITUTE FOR CANCER RESEARCH (US); Licentia OY (FI)

1. .45
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

52.1%; Score 14.6; DB 6; Length 45;
 milarity 81.0%; Pred. No. 8.9e+04;
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCATCTGTCATGGTCA 25
 ||| ||||| ||||| |||||
 ATATCTGTCATGGTCA 26

14359 45 bp DNA linear PAT 11-SEP-2001
 uence 9 from Patent WO0162942.

14359
 14359.1 GI:15593360

thetic construct
 thetic construct
 ificial sequences.

talo, K.M. and Jeltsch, M.M.
 erials and methods involving hybrid vascular endothelial growth
 or dnas and proteins and screening methods for modulators
 nt: WO 0162942-A 9 30-AUG-2001;
 NIG INSTITUTE FOR CANCER RESEARCH (US); Licentia OY (FI)

1. .46
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

52.1%; Score 14.6; DB 6; Length 46;
 milarity 81.0%; Pred. No. 8.9e+04;
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCATCTGTCATGGTCA 25

Db 45 TCATAATCTGCATGGTCA 25
 ||| ||||| ||||| |||||
 RESULT 34
 AX165131/c
 LOCUS AX165131 DNA linear PAT
 DEFINITION Sequence 326 from Patent WO0138586.
 ACCESSION AX165131
 VERSION AX165131.1 GI:14545960
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho

REFERENCE 1
 AUTHORS Shimkets, R.A. and Leach, M.
 TITLE Nucleic acids containing single nucleotide polymorphism
 methods of use thereof
 JOURNAL Patent: WO 0138586-A 326 31-MAY-2001;
 Curagen Corporation (US)

FEATURES
 source
 1. .51
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

variation

26
 /note="single nucleotide polymorphism"
 Accession number cg43930957"

ORIGIN

Query Match 52.1%; Score 14.6; DB 6; Length 51;
 Best Local Similarity 81.0%; Pred. No. 9e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0;

QY 7 ATCTCTGTCATGGTCA 27
 ||||| ||||| ||||| |||||

Db 49 ATCTCTGTCATGGTCA 29
 ||||| ||||| ||||| |||||

RESULT 35
 AR028646/c

LOCUS AR028646 26 bp DNA linear PAT
 DEFINITION Sequence 14 from patent US 5858740.
 ACCESSION AR028646
 VERSION AR028646.1 GI:5940619

KEYWORDS
 SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 26)

AUTHORS Finer, M.H.; Roberts, M.R.; Dull, T.J.; Zsebo, K.M.; Qin, L.
 Farson, D.A.
 TITLE Method for production of high titer virus and high effec
 retroviral mediated transduction of mammalian cells

JOURNAL Patent: US 5858740-A 14 12-JAN-1999;
 FEATURES Location/Qualifiers
 source 1. .26
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 51.4%; Score 14.4; DB 6; Length 26;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;
 Matches 18; Conservative 0; Mismatches 6; Indels 0;

QY 5 TCATCTCTGTCATGGTCA 28
 ||||| ||||| ||||| |||||

Db 25 TCATCTCTGTCATGGTCA 2
 ||||| ||||| ||||| |||||

RESULT 36
 AR053739/c

53739 26 bp DNA linear PAT 29-SEP-1999
 Source: US 5834256.
 53739.1 GI:5978601
 nown.
 nown.
 lassified.
 (bases 1 to 26)
 er,M.H., Roberts,M.R., Dull,T.J., Zsebo,K.M., Qin,L. and
 son,D.A.
 nod for production of high titer virus and high efficiency
 rovirai mediated transduction of mammalian cells
 ent: US 5834256-A 14 10-NOV-1998;
 Location/Qualifiers
 1..26
 /organism="unknown"
 /mol_type="unassigned DNA"

51.4%; Score 14.4; DB 6; Length 26;
 ilarity 75.0%; Pred. No. 1.1e+05;
 Conservative 0; Mismatches 6; Indels 0;
 ATCCTCTGCATGTCAGGTTCAT 28
 |||||
 TACCTTCTTCAAGGTCAGATCTT 2

6239 26 bp DNA linear PAT 08-AUG-2001
 Source: US 6218187.
 6239.1 GI:15109428
 nown.
 nown.
 assified.
 bases 1 to 26)
 r,M.H., Dull,T.J., Zsebo,K.M., Cooke,K. and Farson,D.A.
 od for production of high titer virus and high efficiency
 oviral mediated transduction of mammalian cells
 nt: US 6218187-A 14 17-APR-2001;
 Location/Qualifiers
 1..26
 /organism="unknown"
 /mol_type="unassigned DNA"

51.4%; Score 14.4; DB 6; Length 26;
 ilarity 75.0%; Pred. No. 1.1e+05;
 Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 ATCCTCTGCATGTCAGGTTCAT 28
 |||||
 ACCTTCTTCAAGGTCAGATCTT 2

8189 26 bp DNA linear PAT 20-APR-2002
 Source: US 6319494.
 8189.1 GI:20219327
 nown.
 nown.
 assified.
 bases 1 to 26)
 r,D.J., Weiss,A., Irving,B.A., Roberts,M.R. and Zsebo,K.
 eric chains for receptor-associated signal transduction
 ways

JOURNAL Patent: US 6319494-A 8 20-NOV-2001;
 FEATURES Location/Qualifiers
 source 1..26
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 51.4%; Score 14.4; DB 6; Length 26;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;
 Matches 18; Conservative 0; Mismatches 6; Indels 0;
 QY 5 TCATCCTCTGCATGTCAGGTTCAT 28
 |||||
 Db 25 TCACCTTCTTCAAGGTCAGATCTT 2

RESULT 39
 I73318/c
 LOCUS 26 bp DNA linear PAT
 DEFINITION Sequence 14 from patent US 5686279.
 ACCESSION I73318
 VERSION I73318.1 GI:3009457
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Finer,M.H., Roberts,M.R., Dull,T.J., Zsebo,K.M., Qin,L.
 TITLE Method for production of high titer virus and high effi
 retroviral mediated transduction of mammalian cells
 Patent: US 5686279-A 14 11-NOV-1997;
 Location/Qualifiers
 source 1..26
 /organism="unknown"
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ORIGIN
 Query Match 51.4%; Score 14.4; DB 6; Length 26;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;
 Matches 18; Conservative 0; Mismatches 6; Indels 0;
 QY 5 TCATCCTCTGCATGTCAGGTTCAT 28
 |||||
 Db 25 TCACCTTCTTCAAGGTCAGATCTT 2

RESULT 40
 AR214471/c
 LOCUS 26 bp mRNA linear PAT
 DEFINITION Sequence 8 from patent US 6407221.
 ACCESSION AR214471
 VERSION AR214471.1 GI:23312296
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Capon,D.J., Weiss,A., Irving,B.A., Roberts,M.R. and Zseb
 Chimeric chains for receptor-associated signal transduct
 pathways
 Patent: US 6407221-A 8 18-JUN-2002;
 Location/Qualifiers
 source 1..26
 /organism="unknown"
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ORIGIN
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45.0	68	15	US-10-131-827-4897	Sequence 4897, Ap	C 488	12.4	44.3	32	12	US-10-429-176-2	Sequen
45.0	69	15	US-10-131-827-6451	Sequence 6451, Ap	C 489	12.4	44.3	32	14	US-10-066-960-65	Sequen
45.0	70	15	US-10-131-827-6841	Sequence 6841, Ap	C 490	12.4	44.3	32	14	US-10-037-282-3	Sequen
45.0	71	15	US-10-131-827-8022	Sequence 8022, Ap	C 491	12.4	44.3	32	14	US-10-205-009-136	Sequen
45.0	72	15	US-10-106-658-3483	Sequence 3483, Ap	C 492	12.4	44.3	32	14	US-10-409-565-61	Sequen
45.0	73	60	US-09-908-975-5231	Sequence 5231, Ap	C 493	12.4	44.3	32	14	US-10-223-666-44	Sequen
45.0	74	60	US-09-908-975-5331	Sequence 5331, Ap	C 494	12.4	44.3	32	14	US-10-223-666-187	Sequen
45.0	75	60	US-09-908-975-8343	Sequence 8343, Ap	C 495	12.4	44.3	32	14	US-10-435-750-3	Sequen
45.0	76	60	US-09-908-975-8984	Sequence 8984, Ap	C 496	12.4	44.3	33	10	US-09-227-718-18	Sequen
45.0	77	60	US-09-908-975-9104	Sequence 9104, Ap	C 497	12.4	44.3	33	10	US-09-227-718-19	Sequen
45.0	78	60	US-09-908-975-10546	Sequence 10546, A	C 498	12.4	44.3	33	10	US-09-840-008-18	Sequen
45.0	79	60	US-09-908-975-11700	Sequence 11700, A	C 499	12.4	44.3	33	10	US-09-840-008-19	Sequen
45.0	80	60	US-09-908-975-12148	Sequence 12148, A	C 500	12.4	44.3	34	9	US-09-923-246-57	Sequen
45.0	81	60	US-09-908-975-12284	Sequence 12284, A	C 501	12.4	44.3	34	14	US-10-295-723-57	Sequen
45.0	82	60	US-09-908-975-14548	Sequence 14548, A	C 502	12.4	44.3	35	9	US-09-784-990-2	Sequen
45.0	83	60	US-09-908-975-14717	Sequence 14717, A	C 503	12.4	44.3	35	14	US-10-229-412-2	Sequen
45.0	84	60	US-09-908-975-14936	Sequence 14936, A	C 504	12.4	44.3	36	10	US-09-227-718-20	Sequen
45.0	85	60	US-09-908-975-14968	Sequence 14968, A	C 505	12.4	44.3	36	10	US-09-840-008-20	Sequen
45.0	86	60	US-09-908-975-15019	Sequence 15019, A	C 506	12.4	44.3	36	15	US-10-418-182-71	Sequen
45.0	87	60	US-09-908-975-16123	Sequence 16123, A	C 507	12.4	44.3	38	10	US-09-780-533A-3662	Sequen
45.0	88	60	US-09-908-975-16758	Sequence 16758, A	C 508	12.4	44.3	38	10	US-09-877-478-2624	Sequen
45.0	89	60	US-09-908-975-17416	Sequence 17416, A	C 509	12.4	44.3	38	10	US-09-877-478-3594	Sequen
45.0	90	60	US-09-908-975-21871	Sequence 21871, A	C 510	12.4	44.3	38	12	US-10-342-902-2624	Sequen
45.0	91	60	US-09-908-975-21938	Sequence 21938, A	C 511	12.4	44.3	38	12	US-10-342-902-3594	Sequen
45.0	92	60	US-09-908-975-23182	Sequence 23182, A	C 512	12.4	44.3	39	15	US-10-099-322-313	Sequen
45.0	93	60	US-09-908-975-31778	Sequence 31778, A	C 513	12.4	44.3	41	10	US-09-227-718-21	Sequen
45.0	94	60	US-09-908-975-31944	Sequence 31944, A	C 514	12.4	44.3	41	10	US-09-840-008-21	Sequen
45.0	95	60	US-09-908-975-32100	Sequence 32100, A	C 515	12.4	44.3	41	15	US-10-277-216-273	Sequen
45.0	96	60	US-09-908-975-32325	Sequence 32325, A	C 516	12.4	44.3	41	16	US-10-126-022-273	Sequen
45.0	97	60	US-10-380-584-22	Sequence 22, Appl	C 517	12.4	44.3	43	9	US-09-815-171A-1	Sequen
45.0	98	15	US-09-877-478-6534	Sequence 6534, Ap	C 518	12.4	44.3	45	9	US-09-818-879-6	Sequen
45.0	99	12	US-10-342-902-6534	Sequence 6534, Ap	C 519	12.4	44.3	45	9	US-09-211-755B-6	Sequen
45.0	100	17	US-09-877-478-117	Sequence 117, Appl	C 520	12.4	44.3	45	9	US-09-793-139-6	Sequen
45.0	101	17	US-10-342-902-117	Sequence 117, Appl	C 521	12.4	44.3	47	15	US-10-349-143-1386	Sequen
45.0	102	20	US-10-174-455-19	Sequence 19, Appl	C 522	12.4	44.3	47	15	US-10-349-143-1941	Sequen
45.0	103	20	US-10-348-431-19	Sequence 19, Appl	C 523	12.4	44.3	50	9	US-09-943-722-122	Sequen
45.0	104	25	US-09-810-796-11	Sequence 11, Appl	C 524	12.4	44.3	50	10	US-09-885-731B-14	Sequen
45.0	105	14	US-10-098-263B-33993	Sequence 33993, A	C 525	12.4	44.3	50	12	US-10-182-975-20	Sequen
45.0	106	14	US-10-098-263B-43207	Sequence 43207, A	C 526	12.4	44.3	50	13	US-10-103-002-13	Sequen

44.3	51	9	US-09-995-593A-34	Sequence 34, Appl	600	12.2	43.6	25	14	US-10-060-998-2106	Sequer
44.3	51	15	US-10-418-182-238	Sequence 238, App	601	12.2	43.6	25	14	US-10-060-998-2107	Sequer
44.3	51	15	US-10-428-868-6	Sequence 6, Appl	602	12.2	43.6	25	14	US-10-060-998-2108	Sequer
44.3	52	14	US-10-171-452A-7	Sequence 7, Appl	603	12.2	43.6	25	14	US-10-060-998-2109	Sequer
44.3	52	14	US-10-076-604-68	Sequence 68, Appl	604	12.2	43.6	25	14	US-10-060-998-2110	Sequer
44.3	52	15	US-10-353-708-7	Sequence 7, Appl	605	12.2	43.6	25	14	US-10-060-998-2111	Sequer
44.3	54	9	US-09-858-332-19	Sequence 19, Appl	606	12.2	43.6	25	14	US-10-060-998-2112	Sequer
44.3	54	10	US-09-741-744A-138	Sequence 138, App	607	12.2	43.6	25	14	US-10-060-998-2113	Sequer
44.3	54	14	US-10-371-404-15	Sequence 15, Appl	608	12.2	43.6	25	14	US-10-060-998-2114	Sequer
44.3	54	15	US-10-418-182-272	Sequence 272, App	609	12.2	43.6	25	14	US-10-320-230-29	Sequer
44.3	54	15	US-10-418-182-280	Sequence 280, App	610	12.2	43.6	25	14	US-10-061-201-2275	Sequer
44.3	54	15	US-10-418-182-298	Sequence 298, App	611	12.2	43.6	25	14	US-10-061-201-2276	Sequer
44.3	54	15	US-10-418-182-299	Sequence 299, App	612	12.2	43.6	27	14	US-10-320-230-27	Sequer
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44.3	57	14	US-10-258-825-15	Sequence 15, Appl	614	12.2	43.6	28	9	US-09-986-666-1	Sequer
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44.3	58	14	US-10-219-248-28	Sequence 28, Appl	616	12.2	43.6	28	9	US-09-986-667-1	Sequer
44.3	58	14	US-10-219-247-28	Sequence 28, Appl	617	12.2	43.6	28	9	US-09-986-667-1	Sequer
44.3	59	9	US-09-783-708-9	Sequence 9, Appl	618	12.2	43.6	28	9	US-09-986-667-1	Sequer
44.3	60	8	US-08-785-997-19	Sequence 19, Appl	619	12.2	43.6	29	9	US-09-951-052A-8	Sequer
44.3	60	8	US-08-736-019-167	Sequence 19, Appl	620	12.2	43.6	29	10	US-09-996-263-35	Sequer
44.3	60	10	US-09-387-340-19	Sequence 11, Appl	621	12.2	43.6	29	10	US-09-370-541-11	Sequer
44.3	60	10	US-09-948-193-11	Sequence 11, Appl	622	12.2	43.6	29	12	US-10-601-242-8	Sequer
44.3	60	10	US-09-386-591-19	Sequence 19, Appl	623	12.2	43.6	29	14	US-10-294-957-1	Sequer
44.3	60	10	US-09-908-975-4978	Sequence 4978, App	624	12.2	43.6	29	14	US-10-240-535-21	Sequer
44.3	60	10	US-09-908-975-5535	Sequence 5535, App	625	12.2	43.6	29	14	US-10-352-586-35	Sequer
44.3	60	10	US-09-908-975-7152	Sequence 7152, App	626	12.2	43.6	30	9	US-10-373-456-10	Sequer
44.3	60	10	US-09-908-975-7796	Sequence 7796, App	627	12.2	43.6	30	9	US-09-896-720-11	Sequer
44.3	60	10	US-09-908-975-8600	Sequence 8600, App	628	12.2	43.6	30	15	US-10-125-994A-94	Sequer
44.3	60	10	US-09-908-975-8915	Sequence 8915, App	629	12.2	43.6	30	15	US-10-182-330-126	Sequer
44.3	60	10	US-09-908-975-9576	Sequence 9576, App	630	12.2	43.6	31	10	US-09-942-463-192	Sequer
44.3	60	10	US-09-908-975-11142	Sequence 11142, App	631	12.2	43.6	32	9	US-09-995-297-25	Sequer
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44.3	60	10	US-09-908-975-13197	Sequence 13197, App	634	12.2	43.6	35	9	US-09-823-829-41	Sequer
44.3	60	10	US-09-908-975-14955	Sequence 14955, App	635	12.2	43.6	35	9	US-09-466-035-21	Sequer
44.3	60	10	US-09-908-975-15824	Sequence 15824, App	636	12.2	43.6	35	9	US-09-823-823-41	Sequer
44.3	60	10	US-09-908-975-16984	Sequence 16984, App	637	12.2	43.6	35	10	US-09-530-139-66	Sequer
44.3	60	10	US-09-908-975-18071	Sequence 18071, App	638	12.2	43.6	35	11	US-09-826-509-307	Sequer
44.3	60	10	US-09-908-975-18719	Sequence 18719, App	639	12.2	43.6	36	9	US-09-814-777A-45	Sequer
44.3	60	10	US-09-908-975-31411	Sequence 31411, App	640	12.2	43.6	36	11	US-09-814-777A-83	Sequer
44.3	60	10	US-09-908-975-31621	Sequence 31621, App	641	12.2	43.6	36	11	US-09-826-509-306	Sequer
44.3	17	14	US-10-060-830-225	Sequence 225, App	642	12.2	43.6	36	11	US-09-826-509-309	Sequer
44.3	17	14	US-10-060-830-226	Sequence 226, App	643	12.2	43.6	39	12	US-10-453-827-464	Sequer
44.3	17	14	US-10-060-998-602	Sequence 602, App	644	12.2	43.6	39	12	US-10-453-827-465	Sequer
44.3	17	14	US-10-156-306-5944	Sequence 5944, App	645	12.2	43.6	39	12	US-10-453-827-466	Sequer
44.3	18	14	US-10-098-276A-10	Sequence 10, Appl	646	12.2	43.6	39	12	US-10-453-827-467	Sequer
44.3	18	14	US-10-364-360-13	Sequence 13, Appl	647	12.2	43.6	39	14	US-10-453-827-533	Sequer
44.3	19	14	US-10-005-956-93	Sequence 93, Appl	648	12.2	43.6	40	10	US-10-199-520-6	Sequer
44.3	20	14	US-10-000-864-17	Sequence 17, Appl	649	12.2	43.6	40	10	US-09-918-696-45	Sequer
44.3	20	14	US-10-145-493B-70	Sequence 70, Appl	650	12.2	43.6	40	10	US-09-918-696-45	Sequer
44.3	20	14	US-10-006-430-48	Sequence 48, Appl	651	12.2	43.6	41	14	US-10-043-573-114	Sequer
44.3	20	15	US-10-187-659A-47	Sequence 47, Appl	652	12.2	43.6	41	14	US-10-005-956-238	Sequer
44.3	20	15	US-10-487-659A-111	Sequence 111, App	653	12.2	43.6	45	9	US-09-753-436-46	Sequer
44.3	20	15	US-10-289-762-5100	Sequence 5100, App	654	12.2	43.6	45	14	US-10-276-709-1	Sequer
44.3	20	16	US-10-210-429-56	Sequence 56, Appl	655	12.2	43.6	45	14	US-10-163-942-46	Sequer
44.3	22	14	US-10-210-429-127	Sequence 127, App	656	12.2	43.6	46	10	US-09-860-738C-45	Sequer
44.3	22	14	US-10-267-129-2	Sequence 2, Appl	657	12.2	43.6	47	15	US-10-349-143-891	Sequer
44.3	24	9	US-09-842-930A-7	Sequence 7, Appl	658	12.2	43.6	47	15	US-10-349-143-1869	Sequer
44.3	24	9	US-09-842-930A-33	Sequence 33, Appl	659	12.2	43.6	49	15	US-10-349-143-3197	Sequer
44.3	25	9	US-09-866-108-12932	Sequence 12932, App	660	12.2	43.6	50	15	US-10-148-835-23	Sequer
44.3	25	9	US-09-866-108-12933	Sequence 12933, App	661	12.2	43.6	50	15	US-10-131-827-3564	Sequer
44.3	25	14	US-10-060-830-501	Sequence 501, App	662	12.2	43.6	50	15	US-10-131-827-3564	Sequer
44.3	25	14	US-10-098-263B-37785	Sequence 37785, App	663	12.2	43.6	50	15	US-10-131-827-6719	Sequer
44.3	25	14	US-10-098-263B-39069	Sequence 39069, App	664	12.2	43.6	50	15	US-10-131-827-7109	Sequer
44.3	25	14	US-10-098-263B-44212	Sequence 44212, App	665	12.2	43.6	50	15	US-10-131-827-7258	Sequer
44.3	25	14	US-10-098-263B-51636	Sequence 51636, App	666	12.2	43.6	50	15	US-10-131-827-7403	Sequer
44.3	25	14	US-10-098-263B-61756	Sequence 61756, App	667	12.2	43.6	51	9	US-10-131-827-7482	Sequer
44.3	25	14	US-10-098-263B-78557	Sequence 78557, App	668	12.2	43.6	51	10	US-09-904-599A-5	Sequer
44.3	25	14	US-10-098-263B-94706	Sequence 94706, App	669	12.2	43.6	51	10	US-09-860-738C-44	Sequer
44.3	25	14	US-10-098-263B-107351	Sequence 107351, App	670	12.2	43.6	52	8	US-09-994-064-25	Sequer
44.3	25	14	US-10-098-263B-107352	Sequence 107352, App	671	12.2	43.6	52	9	US-08-781-986A-1925	Sequer
44.3	25	14	US-10-098-263B-107353	Sequence 107353, App	672	12.2	43.6	52	12	US-10-328-624-1925	Sequer
44.3	25	14	US-10-098-263B-107354	Sequence 107354, App	673	12.2	43.6	52	14	US-10-157-305A-16	Sequer

43.6	52	14	US-10-157-391-16	Sequence 16, Appl	746	12	42.9	22	15	US-10-024-212-429	Sequenc
43.6	52	14	US-10-157-096-16	Sequence 16, Appl	747	12	42.9	22	15	US-10-024-212-432	Sequenc
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43.6	52	14	US-10-157-215A-16	Sequence 16, Appl	749	12	42.9	22	15	US-10-024-212-441	Sequenc
43.6	52	14	US-10-157-299-16	Sequence 16, Appl	750	12	42.9	22	15	US-10-024-212-444	Sequenc
43.6	52	14	US-10-154-91B-16	Sequence 16, Appl	751	12	42.9	23	9	US-09-991-003B-5	Sequenc
43.6	52	14	US-10-156-831-16	Sequence 16, Appl	752	12	42.9	23	13	US-10-150-509-3	Sequenc
43.6	52	14	US-10-157-147-16	Sequence 16, Appl	753	12	42.9	23	14	US-10-216-122-143	Sequenc
43.6	52	14	US-10-157-166-16	Sequence 16, Appl	754	12	42.9	24	10	US-09-940-185-2860	Sequenc
43.6	52	14	US-10-156-902-16	Sequence 16, Appl	755	12	42.9	24	14	US-10-190-101-2	Sequenc
43.6	52	14	US-10-157-318-16	Sequence 16, Appl	756	12	42.9	25	9	US-09-866-108-14950	Sequenc
43.6	52	15	US-10-156-811-16	Sequence 16, Appl	757	12	42.9	25	9	US-09-866-108-14951	Sequenc
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43.6	52	15	US-10-157-317-16	Sequence 16, Appl	760	12	42.9	25	9	US-09-866-108-14954	Sequenc
43.6	52	15	US-10-157-339-16	Sequence 16, Appl	761	12	42.9	25	9	US-09-866-108-14955	Sequenc
43.6	54	10	US-09-892-058A-6	Sequence 17, Appl	762	12	42.9	25	9	US-09-920-552-34	Sequenc
43.6	54	14	US-10-191-813-17	Sequence 17, Appl	763	12	42.9	25	14	US-10-215-112-12602	Sequenc
43.6	58	9	US-09-894-927A-7	Sequence 35, Appl	764	12	42.9	25	14	US-10-215-112-12702	Sequenc
43.6	58	9	US-09-981-286A-35	Sequence 16, Appl	765	12	42.9	25	14	US-10-215-112-12916	Sequenc
43.6	58	13	US-10-058-820-16	Sequence 16, Appl	766	12	42.9	25	14	US-10-098-263B-8913	Sequenc
43.6	59	9	US-09-753-436-91	Sequence 91, Appl	767	12	42.9	25	14	US-10-098-263B-13082	Sequenc
43.6	59	14	US-10-163-942-91	Sequence 91, Appl	768	12	42.9	25	14	US-10-098-263B-18229	Sequenc
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43.6	60	10	US-09-908-975-6924	Sequence 6924, Ap	771	12	42.9	25	14	US-10-098-263B-44259	Sequenc
43.6	60	10	US-09-908-975-7435	Sequence 7435, Ap	772	12	42.9	25	14	US-10-098-263B-46397	Sequenc
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43.6	60	10	US-09-908-975-9742	Sequence 9742, Ap	776	12	42.9	25	14	US-10-098-263B-86352	Sequenc
43.6	60	10	US-09-908-975-10200	Sequence 10200, A	777	12	42.9	25	14	US-10-098-263B-94384	Sequenc
43.6	60	10	US-09-908-975-10344	Sequence 10344, A	778	12	42.9	25	14	US-10-098-263B-108575	Sequenc
43.6	60	10	US-09-908-975-11467	Sequence 11467, A	779	12	42.9	25	14	US-10-098-263B-109598	Sequenc
43.6	60	10	US-09-908-975-11974	Sequence 11974, A	780	12	42.9	25	14	US-10-383-201-124	Sequenc
43.6	60	10	US-09-908-975-12567	Sequence 12567, A	781	12	42.9	26	12	US-10-215-457-8	Sequenc
43.6	60	10	US-09-908-975-13241	Sequence 13241, A	782	12	42.9	26	14	US-10-382-942-2	Sequenc
43.6	60	10	US-09-908-975-13455	Sequence 13455, A	783	12	42.9	28	15	US-09-985-911-21	Sequenc
43.6	60	10	US-09-908-975-14441	Sequence 14441, A	784	12	42.9	30	9	US-09-969-748C-54	Sequenc
43.6	60	10	US-09-908-975-14870	Sequence 14870, A	785	12	42.9	30	10	US-10-321-188-22	Sequenc
43.6	60	10	US-09-908-975-15336	Sequence 15336, A	786	12	42.9	30	14	US-09-728-466-26	Sequenc
43.6	60	10	US-09-908-975-15802	Sequence 15802, A	787	12	42.9	36	9	US-09-728-466-28	Sequenc
43.6	60	10	US-09-908-975-17455	Sequence 17455, A	788	12	42.9	36	9	US-09-736-371B-30	Sequenc
43.6	60	10	US-09-908-975-18307	Sequence 18307, A	789	12	42.9	36	14	US-10-119-431-58	Sequenc
43.6	60	10	US-09-908-975-18874	Sequence 18874, A	790	12	42.9	36	15	US-10-463-442-30	Sequenc
43.6	60	10	US-09-908-975-18931	Sequence 18931, A	791	12	42.9	36	15	US-10-179-940-250	Sequenc
43.6	60	10	US-09-908-975-19974	Sequence 19974, A	792	12	42.9	36	15	US-09-037-460-5	Sequenc
43.6	60	10	US-09-908-975-21210	Sequence 21210, A	793	12	42.9	38	12	US-10-037-417-200	Sequenc
43.6	60	10	US-09-908-975-21394	Sequence 21394, A	794	12	42.9	38	12	US-10-344-404-32	Sequenc
43.6	60	10	US-09-908-975-21404	Sequence 21404, A	795	12	42.9	38	14	US-10-216-484-148	Sequenc
43.6	60	10	US-09-908-975-23004	Sequence 23004, A	796	12	42.9	38	14	US-10-156-306-5510	Sequenc
43.6	60	10	US-09-908-975-23082	Sequence 23082, A	797	12	42.9	38	14	US-10-384-933-148	Sequenc
43.6	60	10	US-09-908-975-23488	Sequence 23488, A	798	12	42.9	39	14	US-10-005-956-1551	Sequenc
43.6	60	10	US-09-908-975-31679	Sequence 31679, A	800	12	42.9	39	14	US-10-280-066-224	Sequenc
43.6	60	14	US-10-037-282-117	Sequence 117, App	801	12	42.9	40	9	US-09-951-401-28	Sequenc
43.6	60	14	US-10-150-762-76	Sequence 76, Appl	802	12	42.9	40	9	US-09-922-101-28	Sequenc
43.6	60	14	US-10-244-821-76	Sequence 76, Appl	803	12	42.9	40	9	US-09-951-402-28	Sequenc
43.6	60	14	US-10-222-654-60	Sequence 60, Appl	804	12	42.9	40	10	US-09-862-151-3	Sequenc
43.6	60	14	US-10-435-750-117	Sequence 117, App	805	12	42.9	40	14	US-10-216-484-76	Sequenc
43.6	60	15	US-10-388-329-13	Sequence 13, Appl	806	12	42.9	40	14	US-10-384-933-76	Sequenc
42.9	20	12	US-10-210-172-229	Sequence 229, App	807	12	42.9	40	14	US-10-005-956-677	Sequenc
42.9	20	15	US-10-199-199-54	Sequence 54, Appl	808	12	42.9	41	14	US-10-280-066-226	Sequenc
42.9	20	15	US-10-199-199-123	Sequence 123, App	809	12	42.9	42	14	US-09-925-922-16	Sequenc
42.9	21	10	US-09-232-785-390	Sequence 390, App	810	12	42.9	44	9	US-10-146-835-11	Sequenc
42.9	21	14	US-10-255-568-14	Sequence 14, Appl	811	12	42.9	45	14	US-10-029-436-3	Sequenc
42.9	21	15	US-10-380-931-8	Sequence 8, Appl	812	12	42.9	45	14	US-10-024-677-23	Sequenc
42.9	21	15	US-10-418-182-112	Sequence 112, App	813	12	42.9	45	14	US-10-024-677-24	Sequenc
42.9	21	15	US-10-418-182-124	Sequence 124, App	814	12	42.9	46	9	US-09-848-164-63	Sequenc
42.9	21	15	US-10-396-897-29	Sequence 29, Appl	815	12	42.9	46	9	US-09-848-164-64	Sequenc
42.9	21	15	US-10-349-143-10737	Sequence 10737, A	816	12	42.9	46	9	US-09-900-379-63	Sequenc
42.9	22	14	US-10-096-125-10	Sequence 10, Appl	817	12	42.9	46	9	US-09-900-379-64	Sequenc
42.9	22	14	US-10-032-585-5585	Sequence 5585, Ap	818	12	42.9	46	9		
42.9	22	15	US-10-164-717-8	Sequence 8, Appl	818	12	42.9	46	9		


```

US-10-014-099F-102
; Sequence 102, Application US/10014099F
; Publication No. US20040003420A1
; GENERAL INFORMATION:
; APPLICANT: KUEHN, Ralf
; APPLICANT: FELDER, Susanne
; APPLICANT: SCHWENK, Frieder
; APPLICANT: KUETER-LUKS, Birgit
; APPLICANT: FAUST, Nicole
; TITLE OF INVENTION: Modified Recombinase
; FILE REFERENCE: 012787wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/014,099F
; CURRENT FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: beta-gal 3
US-10-014-099F-102

Query Match          71.4%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0;

QY      7  ATCCTCTGCATGGTCAGGTC 26
        |||||
DB      1  ATCCTCTGCATGGTCAGGTC 20
        |||||

RESULT 3
US-09-908-975-22950
; Sequence 22950, Application US/09908975
; Publication No. US20030165843A1

```

Application US/10359050
US20030186291A1

```

1 FILE REFERENCE: 36888-0005
2 CURRENT APPLICATION NUMBER: US/09/908,975
3 CURRENT FILING DATE: 2001-07-20
4 PRIOR APPLICATION NUMBER: US 60/287,724
5 PRIOR FILING DATE: 2001-05-02
6 PRIOR APPLICATION NUMBER: US 60/221,607
7 PRIOR FILING DATE: 2000-07-28
8 NUMBER OF SEQ ID NOS: 32337
9 SOFTWARE: PatentIn version 3.0
10 SEQ ID NO 22950
11 LENGTH: 60
12 TYPE: DNA
13 ORGANISM: Homo sapiens
14 US-09-908-975-22950

```

NOTATION: Oligonucleotide

matches	21; conservative	0; mismatches	0; indels
Qy	2	GCATCATCTCTGCATGGTCAGGTCAT	28
Db	12	GCCTCATGCTCTTCAGGTCAGTTCT	38

RESULT 4
US-09-908-975-21137
; Sequence 21137, Application US/09908975
; Publication No. US20030165843A1

```

APPLICATION NUMBER: 08/744,590
FILING DATE: 06-NO. US20020042112A1-96
APPLICATION NUMBER: 08/744,481
FILING DATE: 06-NO. US20020042112A1-96
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2004B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8400
TELEFAX: 858-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 318:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 318:
US-09-179-536B-318

Query Match          57.1%; Score 16; DB 9; Length 42;
Best Local Similarity 79.2%; Pred. No. 2.3e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0;

QY      4 ATCATCCTCTGCATGTCAGGTCA 27
Db      1 ATCATCACTGGAAGATCAGGTCA 24
||||| ||| ||| ||| ||| |||
||||| ||| ||| ||| ||| |||

RESULT 6
US-09-297-576A-318
Sequence 318, Application US/09297576A
Publication No. US20030129589A1
GENERAL INFORMATION:
APPLICANT: KOSTER, Hubert
APPLICANT: LITTLE, Daniel P.
APPLICANT: BRAUN, Andreas
APPLICANT: LOUGH, David M.
APPLICANT: XIANG, Guobing
APPLICANT: VAN DEN BOOM, Dirk
APPLICANT: JURINKE, Christian
APPLICANT: RUPPERT, Andreas
TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
NUMBER OF SEQUENCES: 320
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/297,576A
FILING DATE: 07-Jun-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/947,801
FILING DATE: 08-Oct-97
APPLICATION NUMBER: 08/933,792
FILING DATE: 19-Sep-97
APPLICATION NUMBER: 08/787,639
FILING DATE: 23-Jan-97

```

ION NUMBER: 08/786,988
ATE: 23-Jan-97
ION NUMBER: 08/746,055
ATE: 06-NO. US20030129589A1-96
ION NUMBER: 08/746,036
ATE: 06-NO. US20030129589A1-96
ION NUMBER: 08/744,590
ATE: 06-NO. US20030129589A1-96
ION NUMBER: 08/744,481
ATE: 06-NO. US20030129589A1-96
BENT INFORMATION:
aidman, Stephanie L.
ION NUMBER: 33,779
3/DOCKET NUMBER: 24736-2004
ICATION INFORMATION:
858-450-8499
FOR SEQ ID NO: 318:
HARACTERISTICS:
42 base pairs
nucleic acid
MESS: single
: unknown
EPE: cDNA
AL: NO
: NO
EPE: <Unknown>
SOURCE:
118

57.1%; Score 16; DB 10; Length 42;
similarity 79.2%; Pred. No. 2.3e+03;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;
TCATCCTCTGCATGTCAGGTCA 27
|||||
TCATCAACTGGAGATCAGGTCA 24

309/c

. Application US/09908975
1. US20030165843A1
ATION:
OSHAN, Avi
WASSERMAN, Alon
MINTZ, Eli
MINTZ, Liat
AIGLER, Simchon
ENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
ENTION: THAT POPULATE A TRANSCRIPTOME
E: 36688-0005
ICATION NUMBER: US/09/908,975
G DATE: 2001-07-20
ATION NUMBER: US 60/287,724
DATE: 2001-05-02
ATION NUMBER: US 60/221,607
DATE: 2000-07-28
Q ID NOS: 32337
entIn version 3.0
)

omo sapiens
309
55.0%; Score 15.4; DB 10; Length 60;
similarity 94.1%; Pred. No. 4.3e+03;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;
TCTGCATGTCAGGT 25
|||||
TCTGCAGGGTCAGGT 33

RESULT 8
US-09-908-975-12691
; Sequence 12691, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TR
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12691
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-12691

Query Match 55.0%; Score 15.4; DB 10; Length 60;
Best Local Similarity 76.0%; Pred. No. 4.3e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0;

QY 3 CATCATCCTCTGCATGTCAGGTCA 27
|||||
DB 36 CATGGCCCTCTACATCGTCAGGACA 60

RESULT 9
US-09-873-676-71
; Sequence 71, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding molecule
US-09-873-676-71

Query Match 54.3%; Score 15.2; DB 9; Length 33;
Best Local Similarity 85.0%; Pred. No. 5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGCATCATCCTCTGCATGCT 20
|||||
DB 5 AGCCTCCTCATCTGCATGCT 24

RESULT 10

Application US/10403980
US20030176351A1
ATTENTION:
SEWICZ, SUSAN
SPOM, GERALD T.
EFOM, BARBARA S.
ATTENTION: PEPTIDES AND PEPTIDE ANALOGUES DESIGNED FROM A
ATTENTION: DIABETES-ASSOCIATED AUTOANTIGEN, AND METHODS FOR THEIR
ATTENTION: USE IN THE TREATMENT AND PREVENTION OF DIABETES
E: 20149-1-1
CATION NUMBER: US/10/403,980
3 DATE: 2003-03-28
TION NUMBER: 09/375,211
DATE: 1999-08-23
ID NOS: 29
entIn Ver. 2.1

tificial Sequence

ATTENTION: Description of Artificial Sequence: HLA-DR4
ATTENTION: binding peptide encoding SEQ ID NO: 1.

54.3%; Score 15.2; DB 14; Length 39;
ilarity 85.0%; Pred. No. 5.1e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTCTGCATGTCAGTCA 27
|||||
TTCCGATGTCATGTC 24

184
, Application US/09908975
. US20030165843A1
ATTENTION:
OSHAN, Avi
ASSERMAN, Alon
INTZ, Eli
INTZ, Liat
AIGLER, Simchon
ATTENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
ATTENTION: THAT POPULATE A TRANSCRIPTOME
E: 36688-0005
CATION NUMBER: US/09/908,975
G DATE: 2001-07-20
TION NUMBER: US 60/287,724
DATE: 2001-05-02
TION NUMBER: US 60/221,607
DATE: 2000-07-28
ID NOS: 32337
entIn version 3.0
4

mo sapiens
184

54.3%; Score 15.2; DB 10; Length 60;
ilarity 85.0%; Pred. No. 5.3e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTCCTCTGCATGTCAGT 25
|||||
TTCCACTGCTTGGTCAGT 37

236

; Sequence 9236, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 9236
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-9236

Query Match 53.6%; Score 15; DB 14; Length 25;
Best Local Similarity 78.3%; Pred. No. 6e+03; Indels 0;
Matches 18; Conservative 0; Mismatches 5;

QY 6 CATCTCTGCATGTCAGTCA 28
|||||
Db 3 CGTTCCTTCATAGTCAGGCGAT 25

RESULT 13
US-10-221-943-12
; Sequence 12, Application US/10221943
; Publication No. US20040054134A1
; GENERAL INFORMATION:
; APPLICANT: Steinkuhler, Christian
; APPLICANT: Pallaro, Michele
; APPLICANT: Lahm, Armin
; TITLE OF INVENTION: HCV NS2/3 FRAGMENTS AND USES THEREOF
; FILE REFERENCE: IT0031P
; CURRENT APPLICATION NUMBER: US/10/221,943
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: PCT/IB01/0052
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: GB 0006537.5
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-221-943-12

Query Match 53.6%; Score 15; DB 12; Length 44;
Best Local Similarity 78.3%; Pred. No. 6.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0;

QY 2 GCATCATCTCTGCATGTCAGG 24
|||||
Db 2 GCATCATCATCATCATCAGG 24

RESULT 14
US-09-908-975-31738/c
; Sequence 31738, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRA

ENTION: THAT POPULATE A TRANSCRIPTOME

CE: 36688-0005
IGATION NUMBER: US/09/908,975
NG DATE: 2001-07-20
ACTION NUMBER: US 60/287,724
DATE: 2001-05-02
ACTION NUMBER: US 60/221,607
DATE: 2000-07-28
Q ID NOS: 32337
tentIn version 3.0
38

omo sapiens
1738

53.6%; Score 15; DB 10; Length 60;

milarity 78.3%; Pred.No. 6.4e+03;

Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CATCATCTCTGCATGTCAGG 24

||||| ||||| ||||| |||||

CATCACCATCTTCATGTTGAGG 3

1858/c

8, Application US/09908975

C. US20030165843A1

MATION:

HOSHAN, Avi

WASSERMAN, Alon

MINTZ, Eli

MINTZ, Liat

FAIGLER, Simchon

ENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

ENTION: THAT POPULATE A TRANSCRIPTOME

CE: 36688-0005

IGATION NUMBER: US/09/908,975

NG DATE: 2001-07-20

ACTION NUMBER: US 60/287,724

DATE: 2001-05-02

ACTION NUMBER: US 60/221,607

DATE: 2000-07-28

Q ID NOS: 32337

tentIn version 3.0
58

omo sapiens
1858

53.6%; Score 15; DB 10; Length 60;

milarity 78.3%; Pred.No. 6.4e+03;

Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CATCATCTCTGCATGTCAGG 24

||||| ||||| ||||| |||||

CATCACCATCTTCATGTTGAGG 3

19509/c

9, Application US/10098263B

C. US2003010410A1

MATION:

ittman, Michael

ENTION: Human Microarray

CE: 3118.1

IGATION NUMBER: US/10/098,263B

NG DATE: 2003-01-08

ACTION NUMBER: 60/276,759

DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 19509

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-098-263B-19509

Query Match

Best Local Similarity 52.9%; Score 14.8; DB 14; Length 25;

Matches 16; Conservative 0; Mismatches 2; Indels 0;

Qy

9 CCTCTGCATGTCAGGTC 26

||||| ||||| ||||| |||||

Db 25 CCTCTGCATGTCAGGTC 8

RESULT 17

US-10-321-039-297/c

; Sequence 297, Application US/10321039

; Publication No. US20040014067A1

; GENERAL INFORMATION:

; APPLICANT: Lyamichev, Victor

; APPLICANT: Lukowiak, Andrew

; APPLICANT: Jarvis, Nancy

; APPLICANT: Kurensky, David

; TITLE OF INVENTION: Amplification Methods and Compositions

; FILE REFERENCE: FORS-06960

; CURRENT APPLICATION NUMBER: US/10/321,039

; CURRENT FILING DATE: 2002-12-17

; PRIOR APPLICATION NUMBER: 09/998,157

; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/329,113

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/360,489

; PRIOR FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 759

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 297

; LENGTH: 46

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-321-039-297

Query Match

Best Local Similarity 52.9%; Score 14.8; DB 15; Length 46;

Matches 19; Conservative 0; Mismatches 7; Indels 0;

Qy

1 AGCATCATCTCTGCATGTCAGGTC 26

||||| ||||| ||||| |||||

Db 26 AGCATCATCTCTGCATGTCAGGTC 1

RESULT 18

US-10-131-827-1808

; Sequence 1808, Application US/10131827

; Publication No. US20040009479A1

; GENERAL INFORMATION:

; APPLICANT: Wohlgenuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND

; FILE REFERENCE: 506612000120

; CURRENT APPLICATION NUMBER: US/10/131,827

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764

; PRIOR FILING DATE: 2001-06-08

Q ID NOS: 9090
tentIn version 3.1
B

omo sapiens
808

```

52.9%; Score 14.8; DB 15; Length 50;
milarity 88.9%;
Pred. No. 7.7e+03;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTGCATGGTCAGGTCAT 28
|||||
CTGCATGGTCAGGTCAT 40
|||||

```

3378/c
, Application US/10282122A
O. US20040029129A1
MATION:

ang, Liangsung,
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
Xu, H.

ENTION: Identification of Essential Genes in Microorganisms

CE: ELITRA.034A

LOCATION NUMBER: US/10/20	LOCATION NUMBER: US/10/20
DATE: 2003-02-20	DATE: 2003-02-20
ACTION NUMBER: 607191,078	ACTION NUMBER: 607191,078
DATE: 2000-03-21	DATE: 2000-03-21
ACTION NUMBER: 607206,848	ACTION NUMBER: 607206,848
DATE: 2000-05-23	DATE: 2000-05-23
ACTION NUMBER: 607207,727	ACTION NUMBER: 607207,727
DATE: 2000-05-26	DATE: 2000-05-26
ACTION NUMBER: 607230,335	ACTION NUMBER: 607230,335
DATE: 2000-09-06	DATE: 2000-09-06
ACTION NUMBER: 607230,347	ACTION NUMBER: 607230,347
DATE: 2000-09-09	DATE: 2000-09-09
ACTION NUMBER: 607242,578	ACTION NUMBER: 607242,578
DATE: 2000-10-23	DATE: 2000-10-23
ACTION NUMBER: 607253,625	ACTION NUMBER: 607253,625
DATE: 2000-11-27	DATE: 2000-11-27
ACTION NUMBER: 607257,931	ACTION NUMBER: 607257,931
DATE: 2000-12-22	DATE: 2000-12-22
ACTION NUMBER: 607267,636	ACTION NUMBER: 607267,636
DATE: 2001-02-09	DATE: 2001-02-09
ACTION NUMBER: 607269,308	ACTION NUMBER: 607269,308
DATE: 2001-02-16	DATE: 2001-02-16
or Application data removed	or Application data removed
ID NOS: 78614	ID NOS: 78614
Print Version: 3	Print Version: 3

Shcherichia coli
1378

52.9%; Score 14.8; DB 12; Length 53;
 73.1%; Pred. No. 7.7e+03;
 Conservative 0; Mismatches 7; Indels 0; Gaps 0;

5'-CATCATCCTCTGCATGGTCAGGTC-3'

db 28 AGCATCAAGCTCAGCAACGTGAAGTC 3

RESULT 20

```

US-09-908-975-16241/c
; Sequence 16241, Application US/09908975
; Publication No. US2003015843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TF
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36698-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatertIn version 3.0
; SEQ ID NO 16241
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-16241

```

```
Query Match      52.9%;      Score 14.8;  DB 10;  Length 60;
Best Local Similarity 73.1%;      Pred. No. 7.8e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0;
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2 GCATCATCCTCTGCATGGTCAAGTCA 27

45 GCATCATCATCTGGATAGGAAATTC

RESULT 21

```

US-09-908-975-18696
/ Sequence 18696, Application US/09908975
/ Publication NO. US20030165843A1
/ GENERAL INFORMATION:
/ APPLICANT: SHOSHAN, Avi
/ APPLICANT: WASSERMAN, Alon
/ APPLICANT: MINTZ, Eli
/ APPLICANT: MINTZ, Liat
/ APPLICANT: FAIGLER, Simchon
/ TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TR
/ TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
/ FILE REFERENCE: 36888-0005
/ CURRENT APPLICATION NUMBER: US/09/908,975
/ CURRENT FILING DATE: 2001-07-20
/ PRIOR APPLICATION NUMBER: US 60/287,724
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: US 60/221,607
/ PRIOR FILING DATE: 2000-07-28
/ NUMBER OF SEQ ID NOS: 32337
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 18696
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-908-975-18696

```

```
Query Match      52.9%;      Score 14.8;      DB 10;      Length 60;
Best Local Similarity 73.1%;      Pred. No. 7.8e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0;
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3 CATCATCCTCTGCATGGTCAAGTCAAT 28

2 CTTCAATCCACTCCATGCTCAGCAGCT 37
pb

```

-479
; Application US/10074978A
; US20040010119A1
; APPLICATION:
;   Leite, Mario
;   Spytek, Kimberly A
;   Guo, Xiaojia (Sasha)
;   Fernandes, Elma
;   Li, Li
;   Kekuda, Ramesh
;   Liu, Xiahong
;   Casman, Stacie
;   Boldog, Ferenc
;   Patturajan, Meera
;   Blalock, Angela
;   Ballinger, Robert
;   Vernet, Corine
;   Tchernev, Velizar T
;   Gusev, Vladimir
;   Rastelli, Luca
;   Mezes, Peter S
;   Ellerman, Karen
;   Heyes, Melvin P
;   Herzman, John
;   Pena, Carol E A
;   Shimkets, Richard A
;   Taupier Jr, Raymond J
;   Moore, No. US20040010119A111e
;   Edingez, Shlomit
;   Gunther, Erik
;   Stone, Dave
;   Millet, Isabelle
;   Feyman, John
;   Smithson, Glenda
;   TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;   ICE: 21402-269
;   NG DATE: 2003-01-07
;   ACTION NUMBER: 60/268,221
;   ACTION NUMBER: 60/335,109
;   ACTION NUMBER: 60/312,284
;   ACTION NUMBER: 60/268,496
;   ACTION NUMBER: 60/276,703
;   ACTION NUMBER: 60/330,293
;   ACTION NUMBER: 60/310,797
;   ACTION NUMBER: 60/322,127
;   ACTION NUMBER: 60/280,899
;   ACTION NUMBER: 60/268,646
;   Application data removed - See File Wrapper or PALM.
;   Q ID NOS: 547
;   tentIn Ver. 2.1

artificial Sequence
MATION: Description of Artificial Sequence: PCR Primer
MATION: sequence

US-10-074-978A-479
Query Match 52.1%; Score 14.6; DB 15; Length 22;
Best Local Similarity 81.0%; Pred. No. 8.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0

QY 3 CATCATCCTCTGCATGCTCAG 23
Db 1 CCTCATCCTTTTCATGTTTCAG 21

RESULT 23
US-10-074-978A-482
; Sequence 482, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
;   APPLICANT: Leite, Mario
;   APPLICANT: Spytek, Kimberly A
;   APPLICANT: Guo, Xiaojia (Sasha)
;   APPLICANT: Fernandes, Elma
;   APPLICANT: Li, Li
;   APPLICANT: Kekuda, Ramesh
;   APPLICANT: Liu, Xiahong
;   APPLICANT: Casman, Stacie
;   APPLICANT: Boldog, Ferenc
;   APPLICANT: Patturajan, Meera
;   APPLICANT: Blalock, Angela
;   APPLICANT: Ballinger, Robert
;   APPLICANT: Vernet, Corine
;   APPLICANT: Tchernev, Velizar T
;   APPLICANT: Malyankar, Uriel M
;   APPLICANT: Gusev, Vladimir
;   APPLICANT: Rastelli, Luca
;   APPLICANT: Mezes, Peter S
;   APPLICANT: Ellerman, Karen
;   APPLICANT: Heyes, Melvin P
;   APPLICANT: Herzman, John
;   APPLICANT: Pena, Carol E A
;   APPLICANT: Shimkets, Richard A
;   APPLICANT: Taupier Jr, Raymond J
;   APPLICANT: Moore, No. US20040010119A111e
;   APPLICANT: Shenoy, Suresh
;   APPLICANT: Edinger, Shlomit
;   APPLICANT: Gunther, Erik
;   APPLICANT: Stone, Dave
;   APPLICANT: Millet, Isabelle
;   APPLICANT: Peyman, John
;   APPLICANT: Smithson, Glenda
;   TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING S#
;   FILE REFERENCE: 21402-269
;   CURRENT APPLICATION NUMBER: US/10/074,978A
;   CURRENT FILING DATE: 2003-01-07
;   PRIOR APPLICATION NUMBER: 60/268,221
;   PRIOR FILING DATE: 2001-02-12
;   PRIOR APPLICATION NUMBER: 60/335,109
;   PRIOR FILING DATE: 2001-10-31
;   PRIOR APPLICATION NUMBER: 60/312,284
;   PRIOR FILING DATE: 2001-08-14
;   PRIOR APPLICATION NUMBER: 60/268,496
;   PRIOR FILING DATE: 2001-02-13
;   PRIOR APPLICATION NUMBER: 60/276,703
;   PRIOR FILING DATE: 2001-03-16
;   PRIOR APPLICATION NUMBER: 60/330,293
;   PRIOR FILING DATE: 2001-10-18
;   PRIOR APPLICATION NUMBER: 60/322,127
;   PRIOR FILING DATE: 2001-11-21
;   PRIOR APPLICATION NUMBER: 60/280,899
;   PRIOR FILING DATE: 2001-04-02
;   PRIOR APPLICATION NUMBER: 60/310,797
;   PRIOR FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: 60/268,646
;   PRIOR FILING DATE: 2001-02-14
;   Remaining Prior Application data removed - See File Wrapper or P

```

Q ID NOS: 547
tentIn Ver. 2.1

Artificial Sequence

IMATION: Description of Artificial Sequence: PCR Primer
IMATION: sequence

482

milarity 52.1%; Score 14.6; DB 15; Length 22;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCATCTCTGCGATGTCAG 23
|||||
CTCATCTCTGCGATGTCAG 21

93 Application US/10098263B
o. US20030104410A1
MATION:
ittman, Michael
ENTION: Human Microarray
CE: 3118.1
ICATION NUMBER: US/10/098,263B
NG DATE: 2003-01-08
ATION NUMBER: 60/276,759
DATE: 2001-03-16
Q ID NOS: 131066
croarray Probe Sequence Listing Generator V 1.1

omo sapien
93

milarity 52.1%; Score 14.6; DB 14; Length 25;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

GCATCATCTCTGCGATGTC 21
|||||
GCATCGCTCTGCGAAGGTC 24

94 Application US/10098263B
o. US20030104410A1
MATION:
ittman, Michael
ENTION: Human Microarray
CE: 3118.1
ICATION NUMBER: US/10/098,263B
NG DATE: 2003-01-08
ATION NUMBER: 60/276,759
DATE: 2001-03-16
Q ID NOS: 131066
croarray Probe Sequence Listing Generator V 1.1

omo sapien
94

milarity 52.1%; Score 14.6; DB 14; Length 25;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGCATCATCTCTGCGATGTC 21
|||||
Db 4 AGCATCGCATCTGCAAGGTC 24

RESULT 26

US-09-904-099-22
; Sequence 22, Application US/09904099
; Publication No. US20030119092A1
; GENERAL INFORMATION:
; APPLICANT: Shankar, Geetha
; APPLICANT: Munning, Jason N
; APPLICANT: Spencer, Juliet V
; TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 10602-013-999
; CURRENT APPLICATION NUMBER: US/09/904,099
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Primer
; OTHER INFORMATION: Edg 5 receptors
US-09-904-099-22

Query Match 52.1%; Score 14.6; DB 10; Length 34;
Best Local Similarity 81.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0;

QY 6 CATCTCTGCGATGTCAGGTC 26
|||||
Db 1 CATCTACTGCGTGTCAAGTC 21

RESULT 27

US-09-904-099-23/c
; Sequence 23, Application US/09904099
; Publication No. US20030119092A1
; GENERAL INFORMATION:
; APPLICANT: Shankar, Geetha
; APPLICANT: Munning, Jason N
; APPLICANT: Spencer, Juliet V
; TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 10602-013-999
; CURRENT APPLICATION NUMBER: US/09/904,099
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Primer f
; OTHER INFORMATION: Edg 5 receptors
US-09-904-099-23

Query Match 52.1%; Score 14.6; DB 10; Length 34;
Best Local Similarity 81.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0;

QY 6 CATCTCTGCGATGTCAGGTC 26
|||||
Db 34 CATCTACTGCGTGTCAAGTC 14

RESULT 28

US-10-418-182-89/c
; Sequence 89, Application US/10418182
; Publication No. US20030228302A1

ug-10-090-326-23.max.rnpb

```

/ NUMBER OF SEQ ID NOS: 175
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 18
/ LENGTH: 45
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Artificial
/ OTHER INFORMATION: oligonucleotide sequence derived from multip
/ OTHER INFORMATION: endothelial growth factor
US-09-7995-006A-18

```

Query Match 52.1%; Score 14.6; DB 9; Length 45;
Best Local Similarity 81.0%; Pred. No. 9.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels

5 TCATCCTCTGCATGGTCAGGT 25

Qy 5 TCATCCTCTGCATGGTCAGGT 25
Db 6 TCATAATCTGCATGGTCAGGT 26

RESULT 31

US-09-795-006A-9/c
; Sequence 9, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:

```

; APPLICANT: Alitalo et al
;
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCU
;
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
;
; FILE REFERENCE: 28967/35977B
;
; CURRENT APPLICATION NUMBER: US/09/795,006A
;
; CURRENT FILING DATE: 2001-02-26
;
; PRIOR APPLICATION NUMBER: US 60/205,331
;
; PRIOR FILING DATE: 2000-05-18
;
; PRIOR APPLICATION NUMBER: US 60/185,205
;
; PRIOR FILING DATE: 2000-02-25
;
; NUMBER OF SEQ ID NOS: 175
;
; SOFTWARE: Patentin Ver. 2.0

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ORGANISM: Artificial Sequence

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; FEATURE: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: oligonucleotide sequence derived from multiple
; OTHER INFORMATION: endothelial growth factor
US-09-795-006A-9

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Query Match      52.1%; Score 14.6; DB 9; Length 46;
Best Local Similarity 81.0%; Pred. No. 9.3e+03;
Matches 17: Conservative 0; Mismatches 4; Indels 0;
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QY
5 TCATCCTCTGCATGGTCAAGG 25

Dβ
45 TCATAACTCTGCATGGTGATGT 25

RESULT 32
US-09-908-975-6030/c
; Sequence 6030, Application US/09908975
; Publication No. US20030165843A1

```

: GENERAL INFORMATION:
: APPLICANT: SHOSHAN, Avi
: APPLICANT: WASSERMAN, Alon
: APPLICANT: MINTZ, Eli
: APPLICANT: MINTZ, Liat
: APPLICANT: FAIGLER, Simchon
: TITLE OF INVENTION: OLIGONUC
: TITLE OF INVENTION: THAT PO
: FILE REFERENCE: 36698-0005
: CURRENT APPLICATION NUMBER:
: CURRENT FILING DATE: 2001-0
: PRIOR APPLICATION NUMBER: US

```

DATE: 2001-05-02
 ATION NUMBER: US 60/221,607
 DATE: 2000-07-28
 Q ID NOS: 32337
 tentIn version 3.0
 10

omo sapiens
 1030

52.1%; Score 14.6; DB 10; Length 60;
 milarity 81.0%; Pred. No. 9.5e+03;
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;

GCATCATCTCTGTCAGTGC 21
 |||||
 GCTTCATCTCTGTCAGTGC 27

8899/c

9, Application US/09908975
 o. US20030165843A1

MATION:

HOSHAN, Avi

WASSERMAN, Alon

MINTZ, Eli

MINTZ, Liat

FAIGLER, Simchon

ENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
 ENTION: THAT POPULATE A TRANSCRIPTOME

CE: 36688-0005

ICATION NUMBER: US/09/908,975

NG DATE: 2001-07-20

ATION NUMBER: US 60/287,724

DATE: 2001-05-02

ATION NUMBER: US 60/221,607

DATE: 2000-07-28

Q ID NOS: 32337

tentIn version 3.0
 99

omo sapiens

8899

52.1%; Score 14.6; DB 10; Length 60;
 milarity 81.0%; Pred. No. 9.5e+03;
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;

TCTGTCATGTCAGTGCAT 28
 |||||
 TTCTCCAAGTGCAGTGCAT 30

10724/c

t, Application US/10098263B
 o. US20030104410A1

MATION:

ttman, Michael

ENTION: Human Microarray

TE: 3118.1

ICATION NUMBER: US/10/098,263B

NG DATE: 2003-01-08

ATION NUMBER: 60/276,759

DATE: 2001-03-16

ID NOS: 131066

icroarray Probe Sequence Listing Generator V 1.1

14

ORGANISM: Homo sapien
 US-10-098-263B-90724

Query Match 51.4%; Score 14.4; DB 14; Length 25;
 Best Local Similarity 93.8%; Pred. No. 1.1e+04;
 Matches 15; Conservative 0; Mismatches 1; Indels 0

Qy 11 TCTGTCATGTCAGTGC 26
 |||||
 Db 25 TCTGTCATGTCAGTGC 10

RESULT 35

US-10-098-263B-109519

; Sequence 109519, Application US/10098263B

; Publication No. US20030104410A1

; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B

; PRIOR FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/276,759

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 109519

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-098-263B-109519

Query Match 51.4%; Score 14.4; DB 14; Length 25;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0;

Qy 5 TCATCCTCTGTCAGTGCAGTGCAT 28
 |||||
 Db 2 TCTTCTCGGTCAGCTCAGTGCAT 25

RESULT 36

US-09-944-411-14/c

; Sequence 14, Application US/09944411

; Patent No. US20020106799A1

; GENERAL INFORMATION:

; APPLICANT: FINER, MITCHELL H.

; DULL, THOMAS J.

; ZSEBO, KRISTINA M.

; COOKE, KEEGAN

; FARSON, DEBORAH A.

; TITLE OF INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
 VIRUS AND HIGH EFFICIENCY RETROVIRAL M
 OF MAMMALIAN CELLS

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CELL GENESYS, INC.

; STREET: 322 LAKESIDE DRIVE

; CITY: FOSTER CITY

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/944,411

; FILING DATE: 04-Sep-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/914,893

13 09:04:21 2004

us-10-090-326-23.max.rnpb

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FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/258,152
FILING DATE: 10-JUN-1994
APPLICATION NUMBER: US 08/076,299
FILING DATE: 11-JUN-1993
NEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 13.3
COMMUNICATION INFORMATION:
TELEPHONE: 415-349-9600 X131
TELEFAX: 415-349-7392
N FOR SEQ ID NO: 14:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ULE TYPE: DNA (genomic)
NCE DESCRIPTION: SEQ ID NO: 14:
14
51.4%; Score 14.4; DB 9; Length 26;
imilarity 75.0%; Pred. No. 1.1e+04;
; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

TCATCCTCTGCGATGTCAGTTCAT 28
|||||
TCACCTTCTTCAAGGTCAGATCTT 2

3/c
Application US/09759352
320020111474A1
FORMATION:
TANT: CAPON, DANIEL J
WEISS, ARTHUR
IRVING, BRYAN A
ROBERTS, MARGO R
ZSEBO, KRISTINA
OF INVENTION: CHIMERIC CHAINS FOR RECEPTOR-ASSOCIATED
SIGNAL TRANSDUCTION PATHWAYS
OF SEQUENCES: 51
ADDRESS: CELL GENESYS, INC.
TREET: 322 LAKESIDE DRIVE
ITY: FOSTER CITY
TATE: CALIFORNIA
OUNTRY: USA
IP: 94404
ER READABLE FORM:
EDIUM TYPE: Floppy disk
OMPUTER: IBM PC compatible
PERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
T APPLICATION DATA:
APPLICATION NUMBER: US/09759,352
ILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
APPLICATION DATA:
APPLICATION NUMBER: US 08/567,393
ILING DATE: 01-DEC-1995
APPLICATION NUMBER: US 08/475,442
ILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/238,405
ILING DATE: 05-MAY-1994
APPLICATION NUMBER: US 07/988,194
ILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/627,643
ILING DATE: 13-DEC-1990
APPLICATION NUMBER: WO PCT/US91/09431
ILING DATE: 12-DEC-1991
```

```
ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 5.13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)358-9600 X131
TELEFAX: (415)349-7392
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-759-352-8
Query Match 51.4%; Score 14.4; DB 9; Length 26;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0

QY 5 TCATCCTCTGCGATGTCAGTTCAT 28
Db 25 TCACCTTCTTCAAGGTCAGATCTT 2

RESULT 38
US-10-147-299A-22/c
; Sequence 22, Application US/10147299A
; Publication No. US20040058323A1
; GENERAL INFORMATION:
; APPLICANT: KO, ALBERT I.
; APPLICANT: HAAKE, DAVID A.
; APPLICANT: REIS, MITERMAYER GALVAO
; APPLICANT: MATSUNAGA, JAMES
; APPLICANT: CRODA, JULIO HENRIQUE ROSA
; APPLICANT: SIQUEIRA, ISADORA CRISTINA
; APPLICANT: RILEY, LEE W.
; APPLICANT: BAROCCHI, MICHELE
; APPLICANT: YOUNG, TRACY ANN
; TITLE OF INVENTION: PROTEINS WITH REPETITIVE BACTERIAL-IG-LIKE
; FILE REFERENCE: 3673-19
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-147-299A-22

Query Match 51.4%; Score 14.4; DB 12; Length 26;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0;

QY 4 ATCATCCTCTGCGATGTCAGTCA 27
Db 26 ATCATCCTCTGCGCTTTGGAGTCA 3

RESULT 39
US-10-260-516-14/c
; Sequence 14, Application US/10260516
; Publication No. US20030199093A1
; GENERAL INFORMATION:
; APPLICANT: FINER, MITCHELL H.
; APPLICANT: DULL, THOMAS J.
; APPLICANT: ZSEBO, KRISTINA M.
; APPLICANT: COOKE, KEEGAN
```

3 09:04:21 2004

us-10-090-326-23.max.rnpb

```
FARSON, DEBORAH A.
OF INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
OF MAMMALIAN CELLS
OF SEQUENCES: 48
PONDENCE ADDRESS:
DDRESSEE: CELL GENESYS, INC.
TREET: 322 LAKESIDE DRIVE
ITY: FOSTER CITY
TATE: CALIFORNIA
COUNTRY: USA
IP: 94404
ER READABLE FORM:
EDIUM TYPE: Floppy disk
OMPUTER: IBM PC compatible
PERATING SYSTEM: PC-DOS/MS-DOS
FTWARE: Patentin Release #1.0, Version #1.25
T APPLICATION DATA:
PLICATION NUMBER: US/10/260,516
ILING DATE: 01-Oct-2002
LASSIFICATION: <Unknown>
APPLICATION DATA:
PLICATION NUMBER: US/08/914,893
ILING DATE: <Unknown>
PLICATION NUMBER: 08/517,488
ILING DATE: 21-AUG-1995
PLICATION NUMBER: US 08/258,152
ILING DATE: 10-JUN-1994
PLICATION NUMBER: US 08/076,299
ILING DATE: 11-JUN-1993
EY/AGENT INFORMATION:
AME: KRUPEN, KAREN I.
EGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 13.3
MUNICATION INFORMATION:
ELEPHONE: 415-358-9600 X131
ELEFAX: 415-349-7392
FOR SEQ ID NO: 14:
CE CHARACTERISTICS:
ENGTH: 26 base pairs
YPE: nucleic acid
RANDEDNESS: single
POLOGY: linear
LE TYPE: DNA (genomic)
CE DESCRIPTION: SEQ ID NO: 14:
4
51.4%; Score 14.4; DB 14; Length 26;
milarity 75.0%; Pred. No. 1.1e+04;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;
TATCCTCTGCATGTCAGGTGCT 28
TACCTTCTCAAGGTCAGATCTT 2
30
Application US/09801274
0020032319A1
ATION:
argill, Michele
reland, James S.
ander, Eric S.
ANTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
E: 2825.2009-001
ICATION NUMBER: US/09/801,274
G DATE: 2001-03-07
TION NUMBER: US 60/187,510
DATE: 2000-03-07
TION NUMBER: US 60/206,129
DATE: 2000-05-22
} ID NOS: 1802
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-130

Query Match      51.4%; Score 14.4; DB 9; Length 31;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 1; Mismatches 2; Indels 0,

Qy      3 CATCATCTCTGCGATGCT 20
      |||:||||| |||
Db      12 CATCATCTCTGCGATGCT 29
      |||:||||| |||

Search completed: April 12, 2004, 21:42:57
Job time : 143.308 secs
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